



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 153365

TO: Andrew D Kosar
Location: rem/3c04/3c18
Art Unit: 1654
Wednesday, May 18, 2005

Case Serial Number: 10/731921

From: Toby Port

Location: Biotech-Chem Library
REM1-A59

Phone: 272-2523

tohy.port@uspto.gov

Search Notes

Dear Examiner Kosar,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2005, 09:59:56 ; Search time 58 Seconds
(without alignments)
35.316 Million cell updates/sec

Title: US-10-731-921-3

Perfect score: 23

Sequence: 1 GQPR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	30	2 Q91HB7	Q91HB7 tt virus. o
2	23	100.0	31	2 O8VJ21	O8VJ21 mycobacteri
3	23	100.0	34	2 O06618	O06618 mycobacteri
4	23	100.0	34	2 Q7T2W6	Q7T2W6 mycobacteri
5	23	100.0	35	2 Q679Y6	Q679Y6 pan troglod
6	23	100.0	36	2 Q679Y8	Q679Y8 pan troglod
7	23	100.0	39	2 Q9UEU6	Q9UEU6 homo sapien
8	23	100.0	43	1 IM9A RAT	Q9WV97 rattus norv
9	23	100.0	52	2 Q6M2F9	Q6M2F9 homo sapien
10	23	100.0	59	2 Q71V32	Q71V32 rattus norv
11	23	100.0	61	2 Q54820	Q54820 streptomyc
12	23	100.0	62	2 Q6BWM8	Q6BWM8 debaryomyce
13	23	100.0	63	2 Q8U521	Q8U521 agrobacteri
14	23	100.0	65	2 Q8YMW9	Q8YMW9 anabaena sp
15	23	100.0	67	2 Q9K880	Q9K880 bacillus ba
16	23	100.0	72	2 Q7UWU3	Q7UWU3 rhodospirell
17	23	100.0	73	2 Q7PF50	Q7PF50 anopheles g
18	23	100.0	73	2 Q6A863	Q6A863 propionibac
19	23	100.0	73	2 Q80W36	Q80W36 mus musculu
20	23	100.0	74	2 Q7V8P7	Q7V8P7 prochloroco
21	23	100.0	75	2 Q8DH17	Q8DH17 synchococc
22	23	100.0	76	2 Q6TLY2	Q6TLY2 streptomyc
23	23	100.0	77	2 Q7R5L8	Q7R5L8 giardia lam
24	23	100.0	81	2 Q6ESF6	Q6ESF6 oryza sativ
25	23	100.0	81	2 Q8P835	Q8P835 xanthomonas
26	23	100.0	81	2 Q72CR2	Q72CR2 desulfovibr
27	23	100.0	82	2 Q96Q33	Q96Q33 homo sapien
28	23	100.0	82	2 Q9X5W4	Q9X5W4 rhodobacter
29	23	100.0	85	2 Q86T70	Q86T70 homo sapien
30	23	100.0	85	2 Q8S0W2	Q8S0W2 oryza sativ
31	23	100.0	86	2 Q856X1	Q856X1 mycobacteri

32	23	100.0	87	2 Q8WZ93	Q8WZ93 homo sapien
33	23	100.0	87	2 Q7U442	Q7U442 synchococc
34	23	100.0	88	1 GVPB BACME	Q68677 bacillus me
35	23	100.0	89	1 IM9A_HUMAN	Q9Y517 homo sapien
36	23	100.0	89	1 IM9A_MOUSE	Q9W938 mus musculu
37	23	100.0	89	2 Q68V99	Q68V99 uncultured
38	23	100.0	89	2 Q9DSU8	Q9DSU8 ascovirus d
39	23	100.0	90	1 HYPC ECOLI	P24191 escherichia
40	23	100.0	90	2 Q8XG01	Q8XG01 salmonella
41	23	100.0	90	2 Q7CPX9	Q7CPX9 salmonella
42	23	100.0	90	2 Q7W0F6	Q7W0F6 bordetella
43	23	100.0	90	2 Q7W1D7	Q7W1D7 bordetella
44	23	100.0	90	2 Q7WP44	Q7WP44 bordetella
45	23	100.0	91	2 Q8YRZ8	Q8YRZ8 anabaena sp
46	23	100.0	92	2 Q84VP6	Q84VP6 arabidopsis
47	23	100.0	94	2 Q91UP6	Q91UP6 plaemid p
48	23	100.0	95	2 Q8SA29	Q8SA29 oryza sativ
49	23	100.0	96	2 Q9F6C4	Q9F6C4 propionibac
50	23	100.0	98	2 Q7QCD9	Q7QCD9 aeropyrum p
51	23	100.0	98	2 Q9YCI1	Q9YCI1 giardia lam
52	23	100.0	99	2 Q68QC8	Q68QC8 human immun
53	23	100.0	99	2 Q902H7	Q902H7 human immun
54	23	100.0	100	2 Q90DC9	Q90DC9 chimpanzee
55	23	100.0	101	2 Q7PJ39	Q7PJ39 anopheles g
56	23	100.0	101	2 Q7G4Y8	Q7G4Y8 oryza sativ
57	23	100.0	101	2 Q88Q57	Q88Q57 pseudomonas
58	23	100.0	101	2 Q9RWS5	Q9RWS5 deinococcus
59	23	100.0	101	2 Q8UEN1	Q8UEN1 agrobacteri
60	23	100.0	102	2 Q79F64	Q79F64 anabaena va
61	23	100.0	102	2 Q44560	Q44560 anabaena sp
62	23	100.0	102	2 Q8CAG4	Q8CAG4 mus musculu
63	23	100.0	103	2 Q6Z289	Q6Z289 oryza sativ
64	23	100.0	103	2 Q934X9	Q934X9 salmonella
65	23	100.0	103	2 Q6LV85	Q6LV85 photobacter
66	23	100.0	103	2 Q9Q2P0	Q9Q2P0 human herpe
67	23	100.0	104	1 VPR HV2ST	P20884 human immun
68	23	100.0	105	1 VPR HV2SB	P12455 human immun
69	23	100.0	106	2 Q9FTT2	Q9FTT2 oryza sativ
70	23	100.0	106	2 Q9ST59	Q9ST59 arabidopsis
71	23	100.0	106	2 Q92NZ1	Q92NZ1 rhizobium m
72	23	100.0	107	2 Q7R3Y4	Q7R3Y4 giardia lam
73	23	100.0	108	2 Q820P4	Q820P4 nitrosomona
74	23	100.0	109	2 Q9YDJ3	Q9YDJ3 aeropyrum p
75	23	100.0	109	2 Q8S5J0	Q8S5J0 oryza sativ
76	23	100.0	109	2 Q30535	Q30535 pseudomonas
77	23	100.0	109	2 Q91328	Q91328 pseudomonas
78	23	100.0	109	2 Q8CAU8	Q8CAU8 mus musculu
79	23	100.0	111	2 Q6IM28	Q6IM28 drosophila
80	23	100.0	111	2 Q69X79	Q69X79 oryza sativ
81	23	100.0	111	2 Q8KL09	Q8KL09 rhizobium e
82	23	100.0	112	2 Q8L4D1	Q8L4D1 oryza sativ
83	23	100.0	112	2 Q6H5I3	Q6H5I3 oryza sativ
84	23	100.0	113	2 Q7Z2D7	Q7Z2D7 homo sapien
85	23	100.0	113	2 Q8PIK5	Q8PIK5 xanthomonas
86	23	100.0	115	2 Q783I5	Q783I5 neospora
87	23	100.0	115	2 Q9T220	Q9T220 caenorhabdi
88	23	100.0	115	2 Q8Z6T2	Q8Z6T2 salmonella
89	23	100.0	116	2 Q9N0B1	Q9N0B1 macaca fasc
90	23	100.0	117	2 Q745T3	Q745T3 thermus the
91	23	100.0	118	2 Q69JW2	Q69JW2 oryza sativ
92	23	100.0	119	2 Q8NG30	Q8NG30 homo sapien
93	23	100.0	119	2 Q8S438	Q8S438 sorghum bic
94	23	100.0	120	2 Q6EIQ5	Q6EIQ5 bos taurus
95	23	100.0	121	2 Q6BSN1	Q6BSN1 debaryomyce
96	23	100.0	121	2 Q7XMS8	Q7XMS8 oryza sativ
97	23	100.0	122	2 Q9RVZ1	Q9RVZ1 deinococcus
98	23	100.0	123	2 Q73Y14	Q73Y14 mycobacteri
99	23	100.0	124	2 Q65F14	Q65F14 bacillus li
100	23	100.0	124	2 Q8GLS0	Q8GLS0 bruceella eu
101	23	100.0	124	2 Q8BM12	Q8BM12 mus musculu
102	23	100.0	125	2 Q95U14	Q95U14 drosophila
103	23	100.0	126	2 Q86WR6	Q86WR6 homo sapien
104	23	100.0	126	2 Q7PHJ7	Q7PHJ7 anopheles g

105	23	100.0	126	2	Q92241	Q92441 rhizobium m	178	23	100.0	149	2	Q55148	Q55148 synchocyst
106	23	100.0	126	2	Q9K415	Q9K415 streptomyce	179	23	100.0	149	2	Q8Q5E0	Q8Q5E0 chimpanzee
107	23	100.0	127	2	Q75Gw7	Q75Gw7 oryza sativ	180	23	100.0	150	2	Q8UUV6	Q8UUV6 agrobacteri
108	23	100.0	127	2	Q46488	Q46488 leifsonia x	181	23	100.0	150	2	Q8XXF1	Q8XXF1 raietonia s
109	23	100.0	128	2	Q716J3	Q716J3 mycobacteri	182	23	100.0	150	2	Q8Q4Y1	Q8Q4Y1 chimpanzee
110	23	100.0	128	2	Q69WY6	Q69WY6 oryza sativ	183	23	100.0	151	2	P71854	P71854 mycobacteri
111	23	100.0	128	2	Q7CRK6	Q7CRK6 agrobacteri	184	23	100.0	151	2	Q7TW86	Q7TW86 aeryopyrum p
112	23	100.0	128	2	Q881V3	Q881V3 pseudomonas	185	23	100.0	152	2	Q9YFZ5	Q9YFZ5 aeryopyrum p
113	23	100.0	129	2	Q9BZX3	Q9BZX3 homo sapien	186	23	100.0	152	2	Q9N1U1	Q9N1U1 tupaia glis
114	23	100.0	129	2	Q7AX55	Q7AX55 neisseria m	187	23	100.0	152	2	Q9R6K8	Q9R6K8 agrobacteri
115	23	100.0	129	2	P95144	P95144 mycobacteri	188	23	100.0	153	2	Q87ZA9	Q87ZA9 pseudomonas
116	23	100.0	129	2	Q7TZE5	Q7TZE5 mycobacteri	189	23	100.0	153	2	Q9HU57	Q9HU57 pseudomonas
117	23	100.0	129	2	Q9CB30	Q9CB30 mycobacteri	190	23	100.0	154	2	Q96SK9	Q96SK9 homo sapien
118	23	100.0	129	2	Q9JON5	Q9JON5 neisseria m	191	23	100.0	154	2	Q7QUAO	Q7QUAO giardia lam
119	23	100.0	131	2	Q8H5M1	Q8H5M1 oryza sativ	192	23	100.0	154	2	Q848I8	Q848I8 pseudomonas
120	23	100.0	131	2	Q683Q0	Q683Q0 uncultured	193	23	100.0	154	2	Q8PF84	Q8PF84 xanthomonas
121	23	100.0	132	2	Q8BQ19	Q8BQ19 halobacteri	194	23	100.0	155	1	PA2X_HUMAN	PA2X_HUMAN
122	23	100.0	132	2	Q8NH77	Q8NH77 homo sapien	195	23	100.0	155	2	Q6EPL5	Q6EPL5 oryza sativ
123	23	100.0	132	2	Q52889	Q52889 rhizobium m	196	23	100.0	155	2	Q6ZG41	Q6ZG41 oryza sativ
124	23	100.0	132	2	Q9FCX1	Q9FCX1 erwinia amy	197	23	100.0	155	2	Q830F9	Q830F9 enterococcu
125	23	100.0	132	2	Q73UX3	Q73UX3 mycobacteri	198	23	100.0	157	2	Q7SBW3	Q7SBW3 neurospora
126	23	100.0	132	2	Q7UKC4	Q7UKC4 rhodopirell	199	23	100.0	157	2	Q6ZKY5	Q6ZKY5 oryza sativ
127	23	100.0	132	2	Q8BQ19	Q8BQ19 mus musculu	200	23	100.0	157	2	Q9RXG1	Q9RXG1 deinococcus
128	23	100.0	133	2	Q7X2Y4	Q7X2Y4 uncultured	201	23	100.0	157	2	Q8U631	Q8U631 agrobacteri
129	23	100.0	133	2	Q9ZEP9	Q9ZEP9 pseudomonas	202	23	100.0	157	2	Q9JJ33	Q9JJ33 mus musculu
130	23	100.0	133	2	Q72CF3	Q72CF3 desulfovibr	203	23	100.0	159	2	Q6ES35	Q6ES35 oryza sativ
131	23	100.0	134	2	Q8N2U4	Q8N2U4 homo sapien	204	23	100.0	159	2	Q88DX0	Q88DX0 pseudomonas
132	23	100.0	134	2	Q54682	Q54682 lactococcus	205	23	100.0	160	2	Q8H830	Q8H830 oryza sativ
133	23	100.0	135	1	Y274_BUCAI	Y274_BUCAI	206	23	100.0	160	2	Q9L0Y0	Q9L0Y0 streptomyce
134	23	100.0	135	1	Q81Y04	Q81Y04 buchnera ap	207	23	100.0	161	2	Q85679	Q85679 micromonosop
135	23	100.0	135	2	Q624C7	Q624C7 oryza sativ	208	23	100.0	161	2	Q8UBC4	Q8UBC4 agrobacteri
136	23	100.0	135	2	Q7NY82	Q7NY82 chromobacte	209	23	100.0	162	2	Q26526	Q26526 methanobact
137	23	100.0	135	2	Q8CF47	Q8CF47 mus musculu	210	23	100.0	162	2	Q8N2B5	Q8N2B5 homo sapien
138	23	100.0	137	2	Q95UI3	Q95UI3 streptomyce	211	23	100.0	162	2	Q6ZTGS	Q6ZTGS macaca mula
139	23	100.0	137	2	Q82N20	Q82N20 drosophila	212	23	100.0	162	2	Q8HX38	Q8HX38 xanthomonas
140	23	100.0	138	1	PA2_BOTIN	PA2_BOTIN	213	23	100.0	162	2	Q85680	Q85680 xanthomonas
141	23	100.0	138	2	Q9VCZ0	Q9VCZ0 aeropyrum p	214	23	100.0	162	2	Q8PFY1	Q8PFY1 xanthomonas
142	23	100.0	138	2	Q84949	Q84949 salmonella	215	23	100.0	162	2	Q6A5J9	Q6A5J9 propionibac
143	23	100.0	138	2	Q8Z6L8	Q8Z6L8 salmonella	216	23	100.0	162	2	Q9WU17	Q9WU17 mesocricetu
144	23	100.0	139	2	Q7RUE1	Q7RUE1 neurospora	217	23	100.0	163	2	Q6KAI1	Q6KAI1 oryza sativ
145	23	100.0	139	2	Q94221	Q94221 caenorhabdi	218	23	100.0	163	2	Q52169	Q52169 salmonella
146	23	100.0	139	2	Q6Z637	Q6Z637 oryza sativ	219	23	100.0	164	2	Q8BS64	Q8BS64 mus musculu
147	23	100.0	139	2	Q84NW4	Q84NW4 oryza sativ	220	23	100.0	165	2	Q9HHG9	Q9HHG9 halobacteri
148	23	100.0	139	2	Q8YGS2	Q8YGS2 brucella me	221	23	100.0	165	2	Q6NT23	Q6NT23 homo sapien
149	23	100.0	140	1	YK24_PSEAE	YK24_PSEAE	222	23	100.0	165	2	Q84ZG0	Q84ZG0 oryza sativ
150	23	100.0	140	2	Q8GZ25	Q8GZ25 pseudomonas	223	23	100.0	165	2	Q9FJW7	Q9FJW7 arabisidopsis
151	23	100.0	140	2	Q7NF01	Q7NF01 oryza sativ	224	23	100.0	165	2	Q9M2X2	Q9M2X2 arabisidopsis
152	23	100.0	140	2	Q87W37	Q87W37 pseudomonas	225	23	100.0	166	1	ALLA_AGR5	ALLA_AGR5
153	23	100.0	140	2	Q6D4S6	Q6D4S6 erwinia car	226	23	100.0	166	2	Q7QPP7	Q7QPP7 giardia lam
154	23	100.0	140	2	Q87483	Q87483 chimpanzee	227	23	100.0	166	2	Q23694	Q23694 arabisidopsis
155	23	100.0	141	2	Q9MXT1	Q9MXT1 macaca mula	228	23	100.0	166	2	Q8KZ43	Q8KZ43 uncultured
156	23	100.0	141	2	Q7VYB1	Q7VYB1 bordetella	229	23	100.0	166	2	Q8PDL2	Q8PDL2 xanthomonas
157	23	100.0	141	2	Q7WJ76	Q7WJ76 bordetella	230	23	100.0	166	2	Q9DAB3	Q9DAB3 mus musculu
158	23	100.0	141	2	Q9RU64	Q9RU64 deinococcus	231	23	100.0	166	2	Q6INP4	Q6INP4 xenopus lae
159	23	100.0	143	2	Q741M5	Q741M5 mycobacteri	232	23	100.0	167	2	Q9VZ23	Q9VZ23 methanobact
160	23	100.0	143	2	Q9CZ27	Q9CZ27 mus musculu	233	23	100.0	167	2	Q985V9	Q985V9 rhizobium l
161	23	100.0	144	2	Q9HRN7	Q9HRN7 halobacteri	234	23	100.0	168	1	MOAC_DBIRA	MOAC_DBIRA
162	23	100.0	144	2	Q99KS1	Q99KS1 mus musculu	235	23	100.0	168	2	Q8S0M0	Q8S0M0 oryza sativ
163	23	100.0	145	2	Q9UVJ7	Q9UVJ7 aspergillus	236	23	100.0	168	2	Q8H4P3	Q8H4P3 oryza sativ
164	23	100.0	145	2	Q9H2I9	Q9H2I9 pseudomonas	237	23	100.0	168	2	Q7VJTM8	Q7VJTM8 helicobacte
165	23	100.0	146	2	Q9GU56	Q9GU56 heterodera	238	23	100.0	168	2	Q7VXK4	Q7VXK4 bordetella
166	23	100.0	146	2	Q97498	Q97498 oryctolagus	239	23	100.0	168	2	Q7W8Z3	Q7W8Z3 bordetella
167	23	100.0	146	2	Q745H4	Q745H4 mycobacteri	240	23	100.0	168	2	Q7WKD6	Q7WKD6 bordetella
168	23	100.0	146	2	Q88L05	Q88L05 pseudomonas	241	23	100.0	168	2	Q888Q4	Q888Q4 pseudomonas
169	23	100.0	147	2	Q70TE9	Q70TE9 drosophila	242	23	100.0	169	1	CF2A_MOUSE	CF2A_MOUSE
170	23	100.0	147	2	Q55533	Q55533 synchocyst	243	23	100.0	170	1	ALLI_RHIME	ALLI_RHIME
171	23	100.0	147	2	Q8BNP1	Q8BNP1 mus musculu	244	23	100.0	170	2	Q62JH1	Q62JH1 burkholderi
172	23	100.0	148	2	Q9REU8	Q9REU8 pseudomonas	245	23	100.0	170	2	Q63T54	Q63T54 burkholderi
173	23	100.0	148	2	Q743S2	Q743S2 mycobacteri	246	23	100.0	171	2	Q9NPV6	Q9NPV6 homo sapien
174	23	100.0	148	2	Q9CH09	Q9CH09 lactococcus	247	23	100.0	171	2	Q9A4Q2	Q9A4Q2 caulobacter
175	23	100.0	149	2	Q8PU26	Q8PU26 methanobact	248	23	100.0	171	2	Q8C2X6	Q8C2X6 mus musculu
176	23	100.0	149	2	Q6IKD6	Q6IKD6 drosophila	249	23	100.0	172	2	Q8W2X4	Q8W2X4 oryza sativ
177	23	100.0	149	2	Q8GA35	Q8GA35 escherichia	250	23	100.0	172	2	Q6Q1W0	Q6Q1W0 chlamydomon

251	23	100.0	172	2	Q8CEI4	Q8cei4 mus musculus	324	23	100.0	195	2	O89172	O89172 rice grassy
252	23	100.0	174	2	Q9FLI1	Q9fli1 arabidopsis	325	23	100.0	195	2	Q91144	Q91144 rice grassy
253	23	100.0	176	2	Q7TUY0	Q7tuy0 prochloroco	326	23	100.0	195	2	Q91W24	Q91W24 cactus viru
254	23	100.0	176	2	Q87WA2	Q87wa2 pseudomonas	327	23	100.0	196	2	Q8N931	Q8N931 homo sapien
255	23	100.0	176	2	Q9KD61	Q9kd61 bacillus ha	328	23	100.0	196	2	Q8ILF1	Q8ilf1 drosophila
256	23	100.0	176	2	Q9RWL3	Q9rw13 deinococcus	329	23	100.0	196	2	Q9HU79	Q9hu79 pseudomonas
257	23	100.0	177	1	Y254_PYRFU	Q8u441 pyrococcus	330	23	100.0	196	2	Q91ZF0	Q91zf0 mus musculus
258	23	100.0	177	1	Q93311	Q93311 caenorhabdi	331	23	100.0	197	1	ATKC_CAUCR	Q9a7x6 caulobacter
259	23	100.0	178	2	Q82KL4	Q82kl4 streptomyce	332	23	100.0	197	2	Q7QB52	Q7qb52 anopheles g
260	23	100.0	180	1	I17B_HUMAN	Q9uhf5 homo sapien	333	23	100.0	198	2	Q8SS16	Q8ss16 encephalito
261	23	100.0	180	2	Q6IAG3	Q6ia93 homo sapien	334	23	100.0	198	2	Q9P0P4	Q9p0p4 homo sapien
262	23	100.0	180	2	Q82GM2	Q82gm2 streptomyce	335	23	100.0	198	2	Q8HY82	Q8hya2 sus scrofa
263	23	100.0	181	2	Q7KW93	Q7kw93 drosophila	336	23	100.0	198	2	Q48371	Q48371 insertion s
264	23	100.0	182	2	Q6C678	Q6c678 yarrowia li	337	23	100.0	198	2	Q8R614	Q8r614 agrobacteri
265	23	100.0	182	2	Q9TNR3	Q9tnr3 macaca mula	338	23	100.0	198	2	Q8NQN8	Q8nqn8 corynebacte
266	23	100.0	182	2	Q89IJ8	Q89ij8 bradyrhizob	339	23	100.0	198	2	Q98J07	Q98j07 rhizobium l
267	23	100.0	182	2	Q9DX83	Q9dk83 human immun	340	23	100.0	198	2	Q9JUF5	Q9juf5 mus musculus
268	23	100.0	183	2	Q6FS12	Q6fs12 candida gla	341	23	100.0	199	2	Q6A9G7	Q6a9g7 propionbac
269	23	100.0	183	2	Q7SFK1	Q7sfk1 neurospora	342	23	100.0	200	2	Q9C2F1	Q9c2f1 neurospora
270	23	100.0	183	2	Q7SFK1	Q7sfk1 neurospora	343	23	100.0	200	2	Q6IPX3	Q6ipx3 homo sapien
271	23	100.0	184	2	Q8VY57	Q8vy57 arabidopsis	344	23	100.0	200	2	Q97N20	Q97n20 clostridium
272	23	100.0	184	2	Q93V31	Q93v31 arabidopsis	345	23	100.0	201	2	Q7QJ89	Q7qj89 anopheles g
273	23	100.0	184	2	Q6K425	Q6k425 oryza sativ	346	23	100.0	201	2	Q93QF9	Q93qf9 brevbacter
274	23	100.0	184	2	Q7XWY1	Q7xwy1 oryza sativ	347	23	100.0	201	2	Q9R6L7	Q9r6l7 agrobacteri
275	23	100.0	184	2	Q9A897	Q9a897 caulobacter	348	23	100.0	201	2	Q97JF7	Q97jf7 clostridium
276	23	100.0	184	2	Q6D0Z8	Q6d0z8 erwinia car	349	23	100.0	201	2	Q9I6B8	Q9i6b8 pseudomonas
277	23	100.0	184	2	Q9D6D4	Q9d6d4 mus musculus	350	23	100.0	201	2	Q6S865	Q6s865 barley yell
278	23	100.0	185	2	Q18237	Q18237 caenorhabdi	351	23	100.0	201	2	Q8UIX9	Q8uix9 gallus gall
279	23	100.0	185	2	Q96S81	Q96s81 caenorhabdi	352	23	100.0	201	2	Q8UIY0	Q8uiy0 gallus gall
280	23	100.0	185	2	Q86F33	Q86f33 schistosoma	353	23	100.0	201	2	Q76EY7	Q76ey7 gallus gall
281	23	100.0	185	2	Q69909	Q69909 streptomyce	354	23	100.0	202	2	Q92R27	Q92r27 rhizobium m
282	23	100.0	185	2	Q725T8	Q725t8 desulfovibr	355	23	100.0	202	2	Q7VY11	Q7vy11 bordetella
283	23	100.0	185	2	Q82TC6	Q82tc6 nitrosomona	356	23	100.0	202	2	Q7W749	Q7w749 bordetella
284	23	100.0	186	2	Q96BM9	Q96bm9 homo sapien	357	23	100.0	202	2	Q7WIN3	Q7win3 bordetella
285	23	100.0	186	2	Q9NVJ2	Q9nvj2 homo sapien	358	23	100.0	203	2	Q94LH6	Q94lh6 oryza sativ
286	23	100.0	186	2	Q7PQM1	Q7pqm1 anopheles g	359	23	100.0	203	2	Q84R02	Q84r02 oryza sativ
287	23	100.0	186	2	Q9VHV5	Q9vhv5 drosophila	360	23	100.0	203	2	Q9QIX6	Q9qix6 olive leaf
288	23	100.0	186	2	Q8RPT7	Q8rpt7 uncultured	361	23	100.0	204	2	Q6LSD0	Q6lsd0 homo sapien
289	23	100.0	186	2	Q877T9	Q87t9 xylella fas	362	23	100.0	204	2	Q6LSD0	Q6lsd0 photobacter
290	23	100.0	186	2	Q9PCS3	Q9pcs3 xylella fas	363	23	100.0	204	2	Q7U578	Q7u578 bynechococc
291	23	100.0	186	2	Q66HA6	Q66ha6 rattus norv	364	23	100.0	204	2	Q9WZD7	Q9wzd7 thermotoga
292	23	100.0	186	2	Q8VSH3	Q8veh3 mus musculus	365	23	100.0	204	2	Q7TS73	Q7ts73 mus musculus
293	23	100.0	186	2	Q9CQW2	Q9cqw2 m mus muscu	366	23	100.0	205	2	Q87BM2	Q87bm2 xylella fas
294	23	100.0	186	2	Q6NZW8	Q6nzw8 brachydanio	367	23	100.0	205	2	Q9PAT9	Q9pat9 xylella fas
295	23	100.0	186	2	Q6NZ23	Q6nz23 brachydanio	368	23	100.0	205	2	Q9PAU3	Q9pau3 xylella fas
296	23	100.0	186	2	Q6P8C8	Q6p8c8 xenopus tro	369	23	100.0	205	2	Q8QP41	Q8qp41 potato leaf
297	23	100.0	187	2	Q9BVQ2	Q9bvq2 homo sapien	370	23	100.0	206	1	ATKC_XANAC	Q8ppc8 xanthomonas
298	23	100.0	187	2	Q7XSA1	Q7xsa1 oryza sativ	371	23	100.0	206	2	Q96FE3	Q96fe3 homo sapien
299	23	100.0	188	2	Q68834	Q68834 francisella	372	23	100.0	207	1	YQJI_ECOLI	Y64588 escherichia
300	23	100.0	188	2	Q9AGY1	Q9agy1 lactococcus	373	23	100.0	207	1	YQJI_SHIFL	Y64589 shigella fl
301	23	100.0	188	2	Q7NPM7	Q7npw7 chromobacte	374	23	100.0	207	2	Q8MTM3	Q8mtm3 brachiosteo
302	23	100.0	188	2	Q6PBM8	Q6pbm8 brachydanio	375	23	100.0	207	2	Q7DM40	Q7dm40 pinus sylve
303	23	100.0	189	2	Q7WZ71	Q7wz71 bordetella	376	23	100.0	207	2	Q9LY40	Q9ly40 arabidopsis
304	23	100.0	189	2	Q7WR37	Q7wr37 bordetella	377	23	100.0	207	2	Q8FDF9	Q8fd9 escherichia
305	23	100.0	189	2	Q6AC03	Q6ac03 leifsonia x	378	23	100.0	207	2	Q8XAN2	Q8xan2 escherichia
306	23	100.0	190	2	Q96H35	Q96h35 homo sapien	379	23	100.0	207	2	Q9DW27	Q9dw27 rat cytomeg
307	23	100.0	190	2	Q6ZP92	Q6zpz2 homo sapien	380	23	100.0	208	1	COAT_PLRV	Y10470 potato leaf
308	23	100.0	190	2	Q75IA8	Q75ia8 oryza sativ	381	23	100.0	208	1	COAT_PLRV1	Y17522 potato leaf
309	23	100.0	190	2	Q9MX21	Q9mx21 arabidopsis	382	23	100.0	208	1	COAT_PLRV1	Y17521 potato leaf
310	23	100.0	190	2	Q8CBH4	Q8cbh4 mus musculus	383	23	100.0	208	1	COAT_PLRVW	Y11624 potato leaf
311	23	100.0	190	2	Q9CR83	Q9cr83 m mus muscu	384	23	100.0	208	2	Q8N282	Q8n282 homo sapien
312	23	100.0	190	2	Q66J99	Q66j99 xenopus lae	385	23	100.0	208	2	Q9VJF3	Q9vjf3 drosophila
313	23	100.0	191	1	CLP1_CHLCV	Q824c7 chlamydomophi	386	23	100.0	208	2	Q6E3C6	Q6e3c6 oryza sativ
314	23	100.0	191	2	Q9BZV4	Q9bzv4 homo sapien	387	23	100.0	208	2	Q49140	Q49140 methylobact
315	23	100.0	191	2	Q94OL1	Q94ol1 arabidopsis	388	23	100.0	208	2	Q9RV47	Q9rv47 deinococcus
316	23	100.0	191	2	Q7XMK2	Q7xmk2 oryza sativ	389	23	100.0	208	2	Q37936	Q37936 potato leaf
317	23	100.0	191	2	Q9RX62	Q9rx62 deinococcus	390	23	100.0	208	2	Q8QYN7	Q8qyn7 potato leaf
318	23	100.0	191	2	Q90VK2	Q90vk2 human immun	391	23	100.0	208	2	Q8QYP4	Q8qyp4 potato leaf
319	23	100.0	192	2	Q6YWB7	Q6ywb7 oryza sativ	392	23	100.0	208	2	Q8QXQ0	Q8qxq0 potato leaf
320	23	100.0	192	2	Q7P0F9	Q7p0f9 chromobacte	393	23	100.0	208	2	Q8QYR9	Q8qyr9 potato leaf
321	23	100.0	193	2	Q6G4K6	Q6g4k6 bartonella	394	23	100.0	208	2	Q99GS3	Q99gs3 potato leaf
322	23	100.0	194	2	Q7SC18	Q7sc18 neurospora	395	23	100.0	208	2	Q99GS6	Q99gs6 potato leaf
323	23	100.0	195	2	Q52719	Q52719 rhodobacter	396	23	100.0	208	2	Q76QV9	Q76qv9 potato leaf

397	23	100.0	208	2	Q84814	Q84814 potato leaf	470	23	100.0	220	2	Q7QKS4	Q7QKS4 anopheles g
398	23	100.0	208	2	Q84821	Q84821 potato leaf	471	23	100.0	220	2	Q8VLR2	Q8VLR2 bordetella
399	23	100.0	208	2	Q84823	Q84823 potato leaf	472	23	100.0	220	2	Q898P7	Q898P7 rhizobium l
400	23	100.0	208	2	Q84827	Q84827 potato leaf	473	23	100.0	220	2	Q82BH6	Q82BH6 streptomyc
401	23	100.0	208	2	Q84838	Q84838 potato leaf	474	23	100.0	221	2	Q367I7	Q367I7 hordeum vul
402	23	100.0	208	2	Q86898	Q86898 potato leaf	475	23	100.0	221	2	Q9R6T5	Q9R6T5 synchococc
403	23	100.0	208	2	Q8BC79	Q8BC79 potato leaf	476	23	100.0	221	2	Q8YXH1	Q8YXH1 anabaena sp
404	23	100.0	208	2	Q9DKJ1	Q9DKJ1 potato leaf	477	23	100.0	221	2	Q7NEY5	Q7NEY5 gloeobacter
405	23	100.0	208	2	Q9YNY4	Q9YNY4 potato leaf	478	23	100.0	221	2	Q8V4T8	Q8V4T8 monkeypox v
406	23	100.0	209	1	ATKC_XANCP	Q8PCMO xanthomonas	479	23	100.0	222	2	Q6CG04	Q6CG04 yarrowia li
407	23	100.0	209	2	Q8LDR7	Q8LDR7 arabisdopsis	480	23	100.0	222	2	Q67NE7	Q67NE7 symbiobacte
408	23	100.0	209	2	Q8W1L5	Q8W1L5 arabisdopsis	481	23	100.0	222	2	Q8PD41	Q8PD41 xanthomonas
409	23	100.0	209	2	Q9L2M7	Q9L2M7 arabisdopsis	482	23	100.0	222	2	Q8AVA2	Q8AVA2 brachydanio
410	23	100.0	210	2	Q941I3	Q941I3 oryza sativ	483	23	100.0	223	2	Q8IR09	Q8IR09 drosophila
411	23	100.0	210	2	Q7XG29	Q7XG29 oryza sativ	484	23	100.0	223	2	Q61LY3	Q61LY3 drosophila
412	23	100.0	210	2	Q982Z6	Q982Z6 rhizobium l	485	23	100.0	223	2	Q9NHC0	Q9NHC0 drosophila
413	23	100.0	210	2	Q7V8A8	Q7V8A8 prochloroco	486	23	100.0	223	2	Q668I8	Q668I8 yersinia ps
414	23	100.0	211	2	Q8YOV0	Q8YOV0 ralstonia s	487	23	100.0	223	2	Q64TH2	Q64TH2 bacteroides
415	23	100.0	212	1	YQ15_CABEL	Q09230 caenorhabdi	488	23	100.0	223	2	Q8JL79	Q8JL79 ectromelia
416	23	100.0	212	2	Q949Y7	Q949Y7 homo sapien	489	23	100.0	224	1	GPX3_CABEL	Q95003 caenorhabdi
417	23	100.0	212	2	Q71MF6	Q71MF6 homo sapien	490	23	100.0	224	2	Q7PE62	Q7PE62 anopheles g
418	23	100.0	212	2	Q9NTK1	Q9NTK1 homo sapien	491	23	100.0	224	2	Q9B0G1	Q9B0G1 staphylococ
419	23	100.0	212	2	Q7JMK4	Q7JMK4 caenorhabdi	492	23	100.0	224	2	Q91LH7	Q91LH7 arabisdopsis
420	23	100.0	212	2	Q67WM8	Q67WM8 oryza sativ	493	23	100.0	224	2	Q54545	Q54545 escherichia
421	23	100.0	212	2	Q8PQ13	Q8PQ13 xanthomonas	494	23	100.0	224	2	Q823V9	Q823V9 salmonella
422	23	100.0	212	2	Q8C5F6	Q8C5F6 mus musculu	495	23	100.0	224	2	Q90PW7	Q90PW7 chimpanzee
423	23	100.0	213	2	Q9HFP4	Q9HFP4 schizophyll	496	23	100.0	225	2	Q8XCA3	Q8XCA3 escherichia
424	23	100.0	213	2	Q76MX8	Q76MX8 homo sapien	497	23	100.0	225	2	Q6N4G7	Q6N4G7 rhodopseudo
425	23	100.0	213	2	Q9NSM1	Q9NSM1 homo sapien	498	23	100.0	225	2	Q825R9	Q825R9 streptomyc
426	23	100.0	213	2	Q6WAZ5	Q6WAZ5 trypanosoma	499	23	100.0	226	2	Q724Y3	Q724Y3 homo sapien
427	23	100.0	213	2	Q7XTL6	Q7XTL6 oryza sativ	500	23	100.0	226	2	Q54683	Q54683 lactococcus
428	23	100.0	213	2	Q7D766	Q7D766 mycobacteri	501	23	100.0	226	2	P96049	P96049 streptococc
429	23	100.0	213	2	Q53480	Q53480 mycobacteri	502	23	100.0	226	2	Q48649	Q48649 lactococcus
430	23	100.0	213	2	Q7TZ38	Q7TZ38 mycobacteri	503	23	100.0	226	2	Q48653	Q48653 lactococcus
431	23	100.0	213	2	Q7U8Q3	Q7U8Q3 synchococc	504	23	100.0	226	2	Q48716	Q48716 lactococcus
432	23	100.0	213	2	Q9RW35	Q9RW35 deinococcus	505	23	100.0	226	2	Q52090	Q52090 lactococcus
433	23	100.0	213	2	Q6XD14	Q6XD14 sciurus car	506	23	100.0	226	2	Q54350	Q54350 lactococcus
434	23	100.0	214	2	Q623V7	Q623V7 oryza sativ	507	23	100.0	226	2	Q54352	Q54352 lactococcus
435	23	100.0	214	2	Q8PHB3	Q8PHB3 xanthomonas	508	23	100.0	226	2	Q7BLH4	Q7BLH4 lactococcus
436	23	100.0	215	2	Q9NE30	Q9NE30 drosophila	509	23	100.0	226	2	Q7BLP1	Q7BLP1 lactococcus
437	23	100.0	215	2	Q8P5Z5	Q8P5Z5 xanthomonas	510	23	100.0	226	2	Q9L649	Q9L649 lactococcus
438	23	100.0	215	2	Q99JQ3	Q99JQ3 mus musculu	511	23	100.0	226	2	Q9R491	Q9R491 lactococcus
439	23	100.0	216	2	Q9YCU3	Q9YCU3 aeropyrum p	512	23	100.0	226	2	Q9R7J1	Q9R7J1 lactococcus
440	23	100.0	216	2	Q6BM58	Q6BM58 debaryomyce	513	23	100.0	226	2	Q742R4	Q742R4 mycobacteri
441	23	100.0	216	2	Q6FLG6	Q6FLG6 candida gla	514	23	100.0	227	1	EMBP_RAT	Q63189 rattus norv
442	23	100.0	216	2	Q8NSC9	Q8NSC9 homo sapien	515	23	100.0	227	2	Q9HMV3	Q9HMV3 halobacteri
443	23	100.0	216	2	Q6NIA9	Q6NIA9 rhodopseudo	516	23	100.0	227	2	Q6L025	Q6L025 picrophilus
444	23	100.0	217	2	Q754Y4	Q754Y4 ashbya goss	517	23	100.0	227	2	Q7F2F0	Q7F2F0 oryza sativ
445	23	100.0	217	2	Q85613	Q85613 escherichia	518	23	100.0	227	2	Q9ZFX1	Q9ZFX1 pseudomonas
446	23	100.0	217	2	Q7A9R9	Q7A9R9 escherichia	519	23	100.0	227	2	Q63W09	Q63W09 burkholderi
447	23	100.0	217	2	Q6AAB7	Q6AAB7 propionibac	520	23	100.0	228	1	NANE_LACPL	P59441 lactobacill
448	23	100.0	217	2	Q80FI4	Q80FI4 goose hemor	521	23	100.0	228	1	RPIA_RALSO	Q8Y013 ralstonia s
449	23	100.0	218	1	VA41_VARV	P33854 variola vir	522	23	100.0	228	2	Q63613	Q63613 balanogloss
450	23	100.0	218	2	Q8QMR3	Q8QMR3 cowpox viru	523	23	100.0	229	2	Q979E2	Q979E2 thermoplasm
451	23	100.0	218	2	Q85397	Q85397 variola maj	524	23	100.0	229	2	Q9ZX28	Q9ZX28 mycobacteri
452	23	100.0	218	2	Q9QNH4	Q9QNH4 variola min	525	23	100.0	229	2	Q6M463	Q6M463 corynebacte
453	23	100.0	218	2	Q903H6	Q903H6 human immun	526	23	100.0	229	2	Q8XMU6	Q8XMU6 enterococcu
454	23	100.0	219	1	UPPS_AERPE	Q9YCB6 aeropyrum p	527	23	100.0	229	2	Q9D6E8	Q9D6E8 mus musculu
455	23	100.0	219	1	VA41_VACCC	P21064 vaccinia vi	528	23	100.0	230	2	Q8U0G0	Q8U0G0 pyrococcus
456	23	100.0	219	1	VA41_VACCV	P24766 vaccinia vi	529	23	100.0	230	2	Q92290	Q92290 rhizobium m
457	23	100.0	219	2	Q8NYG0	Q8NYG0 staphylococ	530	23	100.0	230	2	Q87DV2	Q87DV2 xylella fas
458	23	100.0	219	2	Q99WU9	Q99WU9 staphylococ	531	23	100.0	230	2	Q9RXX7	Q9RXX7 streptomyc
459	23	100.0	219	2	Q7A7S9	Q7A7S9 staphylococ	532	23	100.0	231	2	Q9HJH9	Q9HJH9 thermoplasm
460	23	100.0	219	2	Q6GCU5	Q6GCU5 staphylococ	533	23	100.0	231	2	Q873D3	Q873D3 neurospora
461	23	100.0	219	2	Q6GK34	Q6GK34 staphylococ	534	23	100.0	231	2	Q9MBS0	Q9MBS0 staphylococ
462	23	100.0	219	2	Q57242	Q57242 vaccinia vi	535	23	100.0	231	2	Q8W4A6	Q8W4A6 arabisdopsis
463	23	100.0	219	2	Q8V2L7	Q8V2L7 camelpox vi	536	23	100.0	231	2	Q7D7K8	Q7D7K8 mycobacteri
464	23	100.0	219	2	Q6RZE2	Q6RZE2 rabbitpox v	537	23	100.0	232	1	DEF_DEIRA	Q9RTQ4 deinococcus
465	23	100.0	219	2	Q76ZN6	Q76ZN6 vaccinia vi	538	23	100.0	232	1	VSR1_BOTJA	P81824 bothrops ja
466	23	100.0	219	2	Q775N8	Q775N8 camelpox vi	539	23	100.0	232	2	Q81X71	Q81X71 methanopyru
467	23	100.0	219	2	Q77TH2	Q77TH2 vaccinia vi	540	23	100.0	232	2	Q87228	Q87228 lactococcus
468	23	100.0	219	2	Q80DT5	Q80DT5 cowpox viru	541	23	100.0	232	2	Q741F6	Q741F6 mycobacteri
469	23	100.0	219	2	Q9IVC3	Q9IVC3 human immun	542	23	100.0	232	2	Q82TK3	Q82TK3 nitrosomona

543	23	100.0	233	2	059233	059233	Pyrococcus	616	23	100.0	250	2	Q87064	Q87064	suid herpes
544	23	100.0	233	2	Q8PYV0	Q8PYV0	methanosaarc	617	23	100.0	250	2	Q84EY8	Q84EY8	pea enation
545	23	100.0	233	2	Q8TIF0	Q8TIF0	methanosaarc	618	23	100.0	251	1	UPPS_VIBVU	Q8dbf7	vibrio vuln
546	23	100.0	233	2	Q8V178	Q8V178	pyrococcus	619	23	100.0	251	1	UPPS_VIBVY	Q7miq4	vibrio vuln
547	23	100.0	233	2	Q8NP51	Q8NP51	corynebacte	620	23	100.0	251	1	Q72C96	Q72c96	desulfovibr
548	23	100.0	234	2	Q6BYW0	Q6BYW0	debaromyce	621	23	100.0	252	1	NXP3_HUMAN	Q95157	homo sapien
549	23	100.0	234	2	Q92SD2	Q92SD2	rhizobium m	622	23	100.0	252	1	NXP3_MOUSE	Q91vx5	mus musculus
550	23	100.0	235	2	Q9SR52	Q9SR52	arabidopsis	623	23	100.0	252	1	NXP3_RAT	Q92n5	rattus norv
551	23	100.0	235	2	Q9JMW6	Q9JMW6	bradyrhizob	624	23	100.0	252	2	Q6ZQR4	Q6zqr4	homo sapien
552	23	100.0	235	2	Q8ZM66	Q8ZM66	salmonella	625	23	100.0	252	2	Q84VC6	Q84vc6	oryza sativ
553	23	100.0	235	2	Q9CU42	Q9CU42	mus musculus	626	23	100.0	252	2	Q92MS9	Q92ms9	rhizobium m
554	23	100.0	236	2	Q54351	Q54351	lactococcus	627	23	100.0	252	2	Q7UK23	Q7uk23	rhodopirell
555	23	100.0	237	2	Q9HN39	Q9HN39	halobacteri	628	23	100.0	252	2	Q7UK24	Q7uk24	rhodopirell
556	23	100.0	237	2	Q9FWM5	Q9FWM5	arabidopsis	629	23	100.0	253	2	Q7USH3	Q7u5h3	synecococc
557	23	100.0	238	2	Q96BP7	Q96BP7	homo sapien	630	23	100.0	253	2	Q9RRZ8	Q9rrz8	deinococcus
558	23	100.0	238	2	Q96D31	Q96D31	homo sapien	631	23	100.0	253	2	Q9D1D1	Q9d1d1	mus muscu
559	23	100.0	238	2	Q96K71	Q96K71	homo sapien	632	23	100.0	254	1	S5A2_PIG	O18765	eus scrofa
560	23	100.0	238	2	Q8H0L2	Q8H0L2	tritium ae	633	23	100.0	254	2	Q8T4Q4	Q8t4q4	aedes aegypt
561	23	100.0	238	2	Q8U7D4	Q8U7D4	agrobacteri	634	23	100.0	254	2	Q8T4Q5	Q8t4q5	aedes aegypt
562	23	100.0	238	2	Q7VWB7	Q7VWB7	bordetella	635	23	100.0	254	2	Q95PA3	Q95pa3	aedes aegypt
563	23	100.0	238	2	Q7W9G9	Q7W9G9	bordetella	636	23	100.0	254	2	Q95PA6	Q95pa6	aedes aegypt
564	23	100.0	238	2	Q7WGZ9	Q7WGZ9	bordetella	637	23	100.0	254	2	Q94GQ5	Q94gq5	oryza sativ
565	23	100.0	238	2	Q87VM1	Q87VM1	pseudomonas	638	23	100.0	254	2	Q7WC99	Q7wc99	bordetella
566	23	100.0	238	2	Q88DG2	Q88DG2	pseudomonas	639	23	100.0	254	2	Q82UW4	Q82uw4	coxiella bu
567	23	100.0	238	2	Q9HUQ4	Q9HUQ4	pseudomonas	640	23	100.0	255	2	Q7CV55	Q7cv55	agrobacteri
568	23	100.0	239	1	6PGL_SYNY3	6PGL_SYNY3	synecocyst	641	23	100.0	255	2	Q6LH36	Q6lh36	photobacter
569	23	100.0	239	2	Q69WM3	Q69WM3	oryza sativ	642	23	100.0	255	2	Q7NR85	Q7nr85	chromobacte
570	23	100.0	239	2	Q8C910	Q8C910	mus musculus	643	23	100.0	255	2	Q9RZP2	Q9rzp2	deinococcus
571	23	100.0	240	2	Q8SOH2	Q8SOH2	oryza sativ	644	23	100.0	255	2	Q8VCL2	Q8vcl2	mus musculu
572	23	100.0	240	2	Q8VX02	Q8VX02	mycobacteri	645	23	100.0	256	1	ATPF_MOUSE	Q8vcq7	mus musculu
573	23	100.0	240	2	Q72HH7	Q72HH7	thermus the	646	23	100.0	256	1	ATPF_RAT	P19511	rattus norv
574	23	100.0	241	2	Q8H4H6	Q8H4H6	oryza sativ	647	23	100.0	256	2	Q92VY2	Q92vy2	rhizobium m
575	23	100.0	241	2	Q9ZSU0	Q9ZSU0	oryza sativ	648	23	100.0	256	2	Q90LS3	Q90ls3	human immun
576	23	100.0	241	2	Q6ZZW6	Q6ZZW6	streptomyce	649	23	100.0	257	2	Q7NR11	Q7nr11	chromobacte
577	23	100.0	241	2	Q8DJZ4	Q8DJZ4	synecococc	650	23	100.0	258	1	VSP2_TRIJE	Q8df67	trimeresuru
578	23	100.0	241	2	Q6AFJ4	Q6AFJ4	desulfotale	651	23	100.0	258	2	Q96K19	Q96k19	homo sapien
579	23	100.0	242	2	Q8DH96	Q8DH96	synecococc	652	23	100.0	258	2	Q92XH6	Q92xh6	rhizobium m
580	23	100.0	242	2	Q9D5A5	Q9D5A5	mus musculus	653	23	100.0	258	2	Q7U4F8	Q7u4f8	synecococc
581	23	100.0	243	1	RS3_SYNP6	RS3_SYNP6	synecococc	654	23	100.0	258	2	Q90ZN2	Q90zn2	gallus gall
582	23	100.0	243	1	Y91Z_MERJA	Y91Z_MERJA	methanococc	655	23	100.0	259	2	Q6L203	Q6l203	picrophilus
583	23	100.0	243	1	ZIPA_XANAC	ZIPA_XANAC	xanthomonas	656	23	100.0	259	2	Q8BWS5	Q8bws5	vibrio vuln
584	23	100.0	243	1	Q6S8A8	Q6S8A8	comamonas s	657	23	100.0	260	1	VSP2_TRIFL	O13057	trimeresuru
585	23	100.0	243	2	Q7W6U7	Q7W6U7	bordetella	658	23	100.0	260	1	VSPA_TRIGA	O13060	trimeresuru
586	23	100.0	243	2	Q7WHT5	Q7WHT5	bordetella	659	23	100.0	260	2	Q9UG54	Q9ug54	homo sapien
587	23	100.0	243	2	Q9PFD1	Q9PFD1	xylella fas	660	23	100.0	260	2	Q8XQ22	Q8xq22	raistonia s
588	23	100.0	244	2	Q61763	Q61763	caenorhabdi	661	23	100.0	260	2	Q88F08	Q88fu8	pseudomonas
589	23	100.0	244	2	Q8Z1U5	Q8Z1U5	salmonella	662	23	100.0	260	2	Q9HXM0	Q9hxm0	pseudomonas
590	23	100.0	245	1	C1QA_MOUSE	C1QA_MOUSE	mus musculus	663	23	100.0	260	2	Q71Q10	Q71q10	trimeresuru
591	23	100.0	245	1	XJBG_ECOLI	XJBG_ECOLI	escherichia	664	23	100.0	261	2	O24230	O24230	oryza sativ
592	23	100.0	245	2	Q7QD70	Q7QD70	anopheles g	665	23	100.0	261	2	Q9AV20	Q9av20	oryza sativ
593	23	100.0	245	2	Q40512	Q40512	nicotiana t	666	23	100.0	261	2	Q8LJU3	Q8lju3	bordetella
594	23	100.0	245	2	Q9SDM1	Q9SDM1	hordeum vul	667	23	100.0	261	2	P74291	P74291	synecocyst
595	23	100.0	245	2	Q8ZK12	Q8ZK12	salmonella	668	23	100.0	261	2	Q6VY34	Q6vy34	turkey astr
596	23	100.0	245	2	Q74110	Q74110	mycobacteri	669	23	100.0	262	2	Q8L3X8	Q8l3x8	arabidopsis
597	23	100.0	245	2	Q89K04	Q89K04	bradyrhizob	670	23	100.0	262	2	Q9FYA9	Q9fya9	arabidopsis
598	23	100.0	245	2	Q8CV17	Q8CV17	escherichia	671	23	100.0	262	2	Q87818	Q87818	roseobacter
599	23	100.0	245	2	Q831P2	Q831P2	shigella fl	672	23	100.0	262	2	Q98LJ1	Q98lj1	rhizobium l
600	23	100.0	245	2	Q9X5X9	Q9X5X9	escherichia	673	23	100.0	262	2	Q88D49	Q88d49	pseudomonas
601	23	100.0	245	2	Q9DCM6	Q9DCM6	mus muscu	674	23	100.0	263	1	SSB_THETH	O85824	thermus the
602	23	100.0	246	1	CB11_LYCES	CB11_LYCES	lycopersico	675	23	100.0	263	2	Q619R6	Q619r6	homo sapien
603	23	100.0	246	2	Q02069	Q02069	pinus sylve	676	23	100.0	263	2	Q70M05	Q70m05	thermus the
604	23	100.0	246	2	Q9FY07	Q9FY07	pisum sativ	677	23	100.0	263	2	Q8XRG2	Q8xrg2	raistonia s
605	23	100.0	246	2	Q6N979	Q6N979	rhodopsedu	678	23	100.0	263	2	Q92VA5	Q92va5	rhizobium m
606	23	100.0	246	2	Q89IF6	Q89IF6	bradyrhizob	679	23	100.0	263	2	Q72GV7	Q72gv7	thermus the
607	23	100.0	247	2	Q86486	Q86486	streptomyce	680	23	100.0	263	2	Q7UUN7	Q7ujn7	rhodopirell
608	23	100.0	247	2	Q988V3	Q988V3	rhizobium l	681	23	100.0	263	2	Q82BQ9	Q82bg9	streptomyce
609	23	100.0	247	2	Q7NSP7	Q7NSP7	chromobacte	682	23	100.0	264	1	LE34_GOSHI	P09444	gossypium h
610	23	100.0	248	2	Q92ZB2	Q92ZB2	rhizobium m	683	23	100.0	264	1	SSB_THERAQ	Q9kh06	thermus aqu
611	23	100.0	248	2	Q73TX5	Q73TX5	mycobacteri	684	23	100.0	264	2	Q81T87	Q8iy87	homo sapien
612	23	100.0	249	2	Q82V15	Q82V15	nitrosomona	685	23	100.0	264	2	Q63MM9	Q63mm9	burkholderi
613	23	100.0	249	2	Q81010	Q81010	mus musculus	686	23	100.0	265	2	Q61218	Q61218	caenorhabdi
614	23	100.0	250	2	Q8BP67	Q8BP67	uncultured	687	23	100.0	265	2	Q9RHH3	Q9rhh3	porphyromon
615	23	100.0	250	2	Q84696	Q84696	pea enation	688	23	100.0	265	2	Q64RU7	Q64ru7	bacteroides

689	23	100.0	265	2	Q8PQ61	Q8PQ61 xanthomonas	762	23	100.0	283	2	Q7CRQ0	Q7CRQ0 agrobacteri
690	23	100.0	265	2	Q8UB74	Q8UB74 agrobacteri	763	23	100.0	283	2	Q8G9K1	Q8G9K1 uncultured
691	23	100.0	265	2	Q6LUJ7	Q6LUJ7 photobacter	764	23	100.0	283	2	Q8XPR3	Q8XPR3 ralstonia s
692	23	100.0	265	2	Q72FZ8	Q72FZ8 desulfovibr	765	23	100.0	283	2	Q97CW7	Q97CW7 clostridium
693	23	100.0	266	2	Q9H611	Q9H611 homo sapien	766	23	100.0	284	2	Q8NF86	Q8NF86 homo sapien
694	23	100.0	266	2	Q9XGW2	Q9XGW2 rosa hybrid	767	23	100.0	284	2	Q6F2D3	Q6F2D3 solanum dem
695	23	100.0	266	2	Q46059	Q46059 corynebacte	768	23	100.0	285	2	Q60501	Q60501 cricetus
696	23	100.0	266	2	Q914V8	Q914V8 pseudomonas	769	23	100.0	286	2	Q872G3	Q872G3 neurospora
697	23	100.0	267	2	Q732N2	Q732N2 brachydanio	770	23	100.0	286	2	Q712J0	Q712J0 rattus norv
698	23	100.0	267	2	Q6FF63	Q6FF63 acinetobact	771	23	100.0	286	2	Q8CBG9	Q8CBG9 mus musculu
699	23	100.0	268	2	Q6NKA8	Q6NKA8 brachydanio	772	23	100.0	287	2	Q9XTT1	Q9XTT1 caenorhabdi
700	23	100.0	269	1	Y374_MYCPN	Y374_MYCPN	773	23	100.0	287	2	Q69X10	Q69X10 oryza sativ
701	23	100.0	269	2	Q7PTI5	Q7PTI5 anopheles g	774	23	100.0	287	2	Q9ZAY6	Q9ZAY6 anabaena sp
702	23	100.0	269	2	Q7R778	Q7R778 plasmodium	775	23	100.0	287	2	Q8VKR7	Q8VKR7 mycobacteri
703	23	100.0	269	2	Q8YU16	Q8YU16 anabaena sp	776	23	100.0	287	2	Q72EU0	Q72EU0 desulfovibr
704	23	100.0	269	2	Q7W070	Q7W070 bordetella	777	23	100.0	287	2	Q7ZUT8	Q7ZUT8
705	23	100.0	270	2	Q7WQA3	Q7WQA3 bordetella	778	23	100.0	288	2	Q52588	Q52588 mycobacteri
706	23	100.0	270	2	Q6RHA6	Q6RHA6 paracoccus	779	23	100.0	289	1	Q9T7_HUMAN	Q9T7_HUMAN
707	23	100.0	271	2	Q86LY6	Q86LY6 branchiosto	780	23	100.0	289	2	Q8BVD7	Q8BVD7 mus musculu
708	23	100.0	271	2	Q80611	Q80611 arabidopsis	781	23	100.0	289	2	Q9Z4Z2	Q9Z4Z2 streptomyce
709	23	100.0	271	2	Q942X1	Q942X1 oryza sativ	782	23	100.0	290	1	GC3_HUMAN	GC3_HUMAN
710	23	100.0	271	2	Q6QF95	Q6QF95 triticum ae	783	23	100.0	290	2	Q6ZAN8	Q6ZAN8 oryza sativ
711	23	100.0	271	2	Q9Z884	Q9Z884 triticum ae	784	23	100.0	290	2	Q79T09	Q79T09 pseudomonas
712	23	100.0	271	2	Q8GJK5	Q8GJK5 synechococc	785	23	100.0	290	2	Q910X2	Q910X2 pseudomonas
713	23	100.0	271	2	Q828S9	Q828S9 streptomyce	786	23	100.0	291	2	Q75B33	Q75B33 ashbya goss
714	23	100.0	272	1	PROC_PSEAE	P22008 pseudomonas	787	23	100.0	291	2	Q721R5	Q721R5 leptospira
715	23	100.0	272	2	Q933D8	Q933D8 haemophilus	788	23	100.0	291	2	Q89M83	Q89M83 bradyrhizob
716	23	100.0	272	2	Q93T06	Q93T06 haemophilus	789	23	100.0	291	2	Q8EY71	Q8EY71 leptospira
717	23	100.0	272	2	Q93T08	Q93T08 haemophilus	790	23	100.0	292	1	MAUI_PARVE	MAUI_PARVE
718	23	100.0	272	2	Q93T10	Q93T10 haemophilus	791	23	100.0	292	2	Q7QOH8	Q7QOH8 giardia lam
719	23	100.0	272	2	Q8UA67	Q8UA67 agrobacteri	792	23	100.0	292	2	Q9VRR7	Q9VRR7 drosophila
720	23	100.0	272	2	Q8YVX0	Q8YVX0 anabaena sp	793	23	100.0	292	2	Q6H077	Q6H077 fremyella d
721	23	100.0	272	2	Q8B372	Q8B372 mus musculu	794	23	100.0	292	2	Q88IN8	Q88IN8 pseudomonas
722	23	100.0	273	2	Q6QF97	Q6QF97 triticum ae	795	23	100.0	292	2	Q89QZ3	Q89QZ3 bradyrhizob
723	23	100.0	273	2	Q93T07	Q93T07 haemophilus	796	23	100.0	293	2	Q8HZC6	Q8HZC6 macaca sp.
724	23	100.0	273	2	Q93T09	Q93T09 haemophilus	797	23	100.0	293	2	Q9HU10	Q9HU10 pseudomonas
725	23	100.0	274	1	RK2_OENHO	Q9mdu0 cenothea h	798	23	100.0	294	2	Q8N4U8	Q8N4U8 homo sapien
726	23	100.0	274	2	Q7Q305	Q7Q305 anopheles g	799	23	100.0	294	2	Q86WE8	Q86WE8 homo sapien
727	23	100.0	274	2	Q8QN88	Q8QN88 ectocarpus	800	23	100.0	294	2	Q6X3K8	Q6X3K8 pseudomonas
728	23	100.0	275	1	DHPS_HAEIN	P43776 haemophilus	801	23	100.0	294	2	Q8CFT0	Q8CFT0 mus musculu
729	23	100.0	275	2	Q65TY7	Q65TY7 mannhelma	802	23	100.0	295	2	Q9P744	Q9P744 neurospora
730	23	100.0	276	2	Q6FJP7	Q6FJP7 homo sapien	803	23	100.0	296	2	Q9P762	Q9P762 oryza sativ
731	23	100.0	276	2	Q7MI03	Q7MI03 vibrio vuln	804	23	100.0	297	2	Q17437	Q17437 caenorhabdi
732	23	100.0	276	2	Q82EM4	Q82EM4 streptomyce	805	23	100.0	297	2	P17178	P17178 mycobacteri
733	23	100.0	276	2	Q87LZ6	Q87LZ6 vibrio para	806	23	100.0	297	2	Q746H2	Q746H2 thermus the
734	23	100.0	276	2	Q8V0N5	Q8V0N5 planococcus	807	23	100.0	297	2	Q7N6L9	Q7N6L9 photorhabd
735	23	100.0	276	2	Q91K83	Q91K83 banana stre	808	23	100.0	297	2	Q7TYM5	Q7TYM5 mycobacteri
736	23	100.0	277	1	HESA_PLEBO	P46037 plectonema	809	23	100.0	297	2	Q87VL2	Q87VL2 pseudomonas
737	23	100.0	277	2	Q934A2	Q934A2 haemophilus	810	23	100.0	297	2	Q6NY38	Q6NY38 brachydanio
738	23	100.0	277	2	Q760B5	Q760B5 uncultured	811	23	100.0	298	2	Q7QC95	Q7QC95 anopheles g
739	23	100.0	277	2	Q9F1J0	Q9F1J0 enterococc	812	23	100.0	298	2	Q8HBP4	Q8HBP4 bos taurus
740	23	100.0	277	2	Q8YB42	Q8YB42 brucella me	813	23	100.0	298	2	Q8HC24	Q8HC24 bos taurus
741	23	100.0	277	2	Q80WM7	Q80WM7 mus musculu	814	23	100.0	298	2	Q7DDV9	Q7DDV9 agrobacteri
742	23	100.0	278	2	Q6AT60	Q6AT60 oryza sativ	815	23	100.0	298	2	Q8YDJ8	Q8YDJ8 brucella me
743	23	100.0	278	2	Q53937	Q53937 streptomyce	816	23	100.0	298	2	Q7PQ07	Q7PQ07 chromobacte
744	23	100.0	278	2	Q8NZK9	Q8NZK9 streptococc	817	23	100.0	298	2	Q89HC5	Q89HC5 bradyrhizob
745	23	100.0	278	2	Q93YA4	Q93YA4 streptococc	818	23	100.0	298	2	Q8FUU5	Q8FUU5 brucella su
746	23	100.0	278	2	Q9A295	Q9A295 caulobacter	819	23	100.0	299	1	SPAH_ECOL6	SPAH_ECOL6
747	23	100.0	278	2	Q9KU85	Q9KU85 vibrio chol	820	23	100.0	299	2	Q93UB1	Q93UB1 bifidobacte
748	23	100.0	278	2	Q8K603	Q8K603 streptococc	821	23	100.0	299	2	Q46686	Q46686 escherichia
749	23	100.0	278	2	Q8BNV0	Q8BNV0 mus musculu	822	23	100.0	299	2	Q53298	Q53298 escherichia
750	23	100.0	279	2	Q8UHH6	Q8UHH6 agrobacteri	823	23	100.0	299	2	Q6Y3B0	Q6Y3B0 geobacter p
751	23	100.0	279	2	Q9RI67	Q9RI67 streptomyce	824	23	100.0	300	1	ERG3_MYCTU	ERG3_MYCTU
752	23	100.0	280	2	Q8N171	Q8N171 homo sapien	825	23	100.0	300	2	Q986Y1	Q986Y1 rhizobium l
753	23	100.0	281	2	Q7MYI2	Q7MYI2 photorhabd	826	23	100.0	301	2	Q6DHX2	Q6DHX2 homo sapien
754	23	100.0	281	2	Q8DMU0	Q8DMU0 synechococc	827	23	100.0	301	2	Q6A723	Q6A723 caenorhabdi
755	23	100.0	282	2	Q6M5H3	Q6M5H3 corynebacte	828	23	100.0	301	2	Q65U69	Q65U69 mannhelma
756	23	100.0	282	2	Q7DJ7A2	Q7DJ7A2 porphyromon	829	23	100.0	301	2	Q8PDZ1	Q8PDZ1 xanthomonas
757	23	100.0	282	2	Q9R2Q8	Q9R2Q8 bacteroides	830	23	100.0	301	2	Q8PQV9	Q8PQV9 xanthomonas
758	23	100.0	282	2	Q9RHH2	Q9RHH2 porphyromon	831	23	100.0	301	2	Q7UA63	Q7UA63 synechococc
759	23	100.0	282	2	Q69952	Q69952 streptomyce	832	23	100.0	301	2	Q9KZP5	Q9KZP5 streptomyce
760	23	100.0	282	2	Q92P66	Q92P66 rhizobium m	833	23	100.0	302	2	Q8GM49	Q8GM49 zymomonas s
761	23	100.0	282	2	Q8BPS8	Q8BPS8 mus musculu	834	23	100.0	302	2	Q8PF07	Q8PF07 xanthomonas s

835	23	100.0	303	2	O84108	O84108 chlamydia t	908	23	100.0	319	2	Q9F1V0	Q9F1V0 flavobacter
836	23	100.0	303	2	O8BRJ3	O8brj3 mus musculus	909	23	100.0	319	2	Q59531	Q59531 mycobacteri
837	23	100.0	304	2	O8N9R4	O8n9r4 homo sapien	910	23	100.0	319	2	Q6NQO8	Q6n0q8 rhodopseudi
838	23	100.0	304	2	O6PK51	O6pk51 homo sapien	911	23	100.0	319	2	Q7WK04	Q7wk04 bordetella
839	23	100.0	304	2	O8LHB6	O8lhb6 oryza sativ	912	23	100.0	319	2	Q8JCY0	Q8jcy0 human immun
840	23	100.0	304	2	O9XI195	O9xi195 arabidopsis	913	23	100.0	320	2	O8N4Q3	Q8n4q3 homo sapien
841	23	100.0	305	2	O16308	O16308 caenorhabdi	914	23	100.0	320	2	O8N7Q9	Q8n7q9 homo sapien
842	23	100.0	305	2	O8MXR6	O8mxr6 caenorhabdi	915	23	100.0	320	2	Q7PHJ6	Q7phj6 anopheles g
843	23	100.0	305	2	Q7QDQ6	Q7qdq6 anopheles g	916	23	100.0	320	2	O8SAX5	O8sax5 oryza sativ
844	23	100.0	305	2	Q935V5	Q935v5 streptomyc	917	23	100.0	320	2	O69RC7	O69rc7 oryza sativ
845	23	100.0	305	2	Q9FW2	Q9fw2 pseudomonas	918	23	100.0	320	2	O8BGS9	O8bgs9 m mus muscu
846	23	100.0	305	2	O8KB19	O8kb19 chlorobium	919	23	100.0	320	2	Q9CSQ4	Q9csq4 mus musculu
847	23	100.0	305	2	O82J66	O82j66 streptomyc	920	23	100.0	321	2	O88PT6	O88pt6 pseudomonas
848	23	100.0	305	2	Q9CSR2	Q9csr2 mus musculu	921	23	100.0	321	2	O8JB55	O8jb55 human immun
849	23	100.0	306	2	Q98CI1	Q98ci1 rhizobium l	922	23	100.0	322	1	ARG1_PIG	ARG1_jc8 sus scrofa
850	23	100.0	306	2	Q7WD35	Q7wd35 bordetella	923	23	100.0	322	1	ARG1_HUMAN	ARG1_jc8 sus scrofa
851	23	100.0	307	1	PDX1_DEIRA	Pdx1 deir	924	23	100.0	322	1	MYDM_HUMAN	MYDM_jc8 sus scrofa
852	23	100.0	308	1	HEM1_THEAC	Hem1 theac	925	23	100.0	322	1	ARG1_HUMAN	ARG1_jc8 sus scrofa
853	23	100.0	308	2	O6ES50	O6es50 oryza sativ	926	23	100.0	322	2	Q9S7P1	Q9s7p1 oryza sativ
854	23	100.0	308	2	O6M781	O6m781 corynebacte	927	23	100.0	322	2	Q57054	Q57054 synechocyst
855	23	100.0	308	2	O53301	O53301 mycobacteri	928	23	100.0	322	2	Q79F82	Q79f82 synechocyst
856	23	100.0	308	2	O8NSI0	O8nsi0 corynebacte	929	23	100.0	322	2	O8KPV1	O8kpv1 chlorobium
857	23	100.0	308	2	O8YNY0	O8yny0 anabaena sp	930	23	100.0	322	2	O88H91	O88h91 pseudomonas
858	23	100.0	308	2	Q7TXA5	Q7txa5 mycobacteri	931	23	100.0	323	1	ARG1_MOUSE	ARG1_jc8 sus scrofa
859	23	100.0	308	2	O88JH3	O88jh3 pseudomonas	932	23	100.0	323	1	ARG1_RAT	ARG1_jc8 sus scrofa
860	23	100.0	310	2	O8DIP3	O8dip3 synechococc	933	23	100.0	323	2	Q8VNM94	Q8vm94 rhodococcus
861	23	100.0	309	1	KHSE_STRCO	Khse strco	934	23	100.0	323	2	Q59563	Q59563 mycobacteri
862	23	100.0	309	2	Q95XV7	Q95xv7 caenorhabdi	935	23	100.0	323	2	Q7TY20	Q7ty20 mycobacteri
863	23	100.0	309	2	Q9M2T3	Q9m2t3 arabidopsis	936	23	100.0	323	2	Q57Y20	Q57y20 mycobacteri
864	23	100.0	309	2	Q9X7I8	Q9x7i8 pseudomonas	937	23	100.0	324	1	Q6DIU5	Q6diu5 xenopus tro
865	23	100.0	310	2	O8NSE8	O8nse8 homo sapien	938	23	100.0	324	2	Q6NEB1	Q6neb1 rhodopseudi
866	23	100.0	310	2	O9XX39	O9xx39 caenorhabdi	939	23	100.0	324	2	Q827E3	Q827e3 streptomyc
867	23	100.0	310	2	O8YZN7	O8yzn7 anabaena sp	940	23	100.0	325	2	Q17402	Q17402 caenorhabdi
868	23	100.0	311	2	Q8TSS5	Q8tss5 methanosarc	941	23	100.0	325	2	Q55392	Q55392 synechocyst
869	23	100.0	311	2	Q19257	Q19257 caenorhabdi	942	23	100.0	325	2	Q9RUM8	Q9rum8 deinococcus
870	23	100.0	311	2	Q7VM42	Q7vm42 bordetella	943	23	100.0	325	2	Q8R4R6	Q8r4r6 mus musculu
871	23	100.0	311	2	Q7W5J9	Q7w5j9 bordetella	944	23	100.0	325	2	Q68FY1	Q68fy1 rattus norv
872	23	100.0	312	2	Q9N591	Q9n591 caenorhabdi	945	23	100.0	325	2	O9D7J2	O9d7j2 m mus muscu
873	23	100.0	312	2	Q9FR72	Q9fr72 hordeum spo	946	23	100.0	325	2	Q6GNG2	Q6gng2 xenopus lae
874	23	100.0	312	2	Q9FE73	Q9fe73 hordeum spo	947	23	100.0	326	1	GC2_HUMAN	GC2_jc8 sus scrofa
875	23	100.0	312	2	Q9FE74	Q9fe74 hordeum spo	948	23	100.0	326	2	O8NPF5	O8nfh5 homo sapien
876	23	100.0	312	2	Q9FPF2	Q9fpf2 hordeum spo	949	23	100.0	326	2	O8TJD1	O8tdj1 homo sapien
877	23	100.0	312	2	Q9FPF3	Q9fpf3 hordeum spo	950	23	100.0	326	2	Q7Y038	Q7y038 mangifera i
878	23	100.0	312	2	Q9FPF4	Q9fpf4 hordeum spo	951	23	100.0	326	2	O9FXB4	O9fxb4 arabidopsis
879	23	100.0	312	2	Q9FPF5	Q9fpf5 hordeum spo	952	23	100.0	326	2	Q80FI5	Q80fi5 goose hemor
880	23	100.0	312	2	F72585	F72585 synechocyst	953	23	100.0	326	2	Q66IG6	Q66ig6 xenopus tro
881	23	100.0	312	2	Q8CHX9	Q8chx9 mus musculu	954	23	100.0	326	2	Q6IP56	Q6ip56 xenopus lae
882	23	100.0	313	1	QYAM_BACSU	Qyam bacsu	955	23	100.0	326	2	Q98YL3	Q98yl3 human immun
883	23	100.0	313	2	O27528	O27528 methanobact	956	23	100.0	327	1	GC4_HUMAN	GC4_jc8 sus scrofa
884	23	100.0	313	2	O67F56	O67f56 comamonas a	957	23	100.0	327	1	GN1L_HUMAN	GN1L_jc8 sus scrofa
885	23	100.0	313	2	O6A7A8	O6a7a8 propionibac	958	23	100.0	327	2	Q9XTU5	Q9xtu5 caenorhabdi
886	23	100.0	313	2	O8DL64	O8dl64 synechococc	959	23	100.0	327	2	Q6GNA1	Q6gna1 xenopus lae
887	23	100.0	314	1	STO2_CABEL	Sto2 cabel	960	23	100.0	327	2	Q632F0	Q632f0 oncorhynch
888	23	100.0	314	2	O6SH15	O6sh15 caenorhabdi	961	23	100.0	328	2	O6NA51	O6na51 rhodopseudi
889	23	100.0	314	2	P71628	P71628 mycobacteri	962	23	100.0	329	2	Q7R3P4	Q7r3p4 giardia lam
890	23	100.0	314	2	O8YVW0	O8yvw0 anabaena sp	963	23	100.0	330	1	GC1_HUMAN	GC1_jc8 sus scrofa
891	23	100.0	314	2	O6LKH0	O6lkh0 photobacter	964	23	100.0	330	2	Q7Q5R3	Q7q5r3 anopheles g
892	23	100.0	314	2	Q7TXS3	Q7txs3 mycobacteri	965	23	100.0	330	2	O02946	O02946 macaca mula
893	23	100.0	315	2	Q8WSM5	Q8wsms caenorhabdi	966	23	100.0	330	2	O02947	O02947 macaca mula
894	23	100.0	315	2	P74817	P74817 sphingomon	967	23	100.0	330	2	O19356	O19356 macaca mula
895	23	100.0	315	2	Q7CSM9	Q7csm9 agrobacteri	968	23	100.0	330	2	Q88N48	Q88n48 pseudomonas
896	23	100.0	316	1	ARG1_XENIA	Arg1 xenia	969	23	100.0	330	2	Q7ZY96	Q7zy96 xenopus lae
897	23	100.0	316	2	O8PVT1	O8pvt1 methanosarc	970	23	100.0	331	2	O02944	O02944 macaca mula
898	23	100.0	316	2	Q6LJV2	Q6ljv2 photobacter	971	23	100.0	331	2	O02945	O02945 macaca mula
899	23	100.0	317	2	Q7R784	Q7r784 plasmodium	972	23	100.0	331	2	O8RTX8	O8rtx8 uncultured
900	23	100.0	317	2	Q63LT9	Q63lt9 burkholderi	973	23	100.0	332	2	Q860F7	Q860f7 macaca reme
901	23	100.0	317	2	O50655	O50655 mycobacteri	974	23	100.0	332	2	Q860F8	Q860f8 macaca reme
902	23	100.0	317	2	Q7TWG4	Q7twg4 mycobacteri	975	23	100.0	332	2	Q73W34	Q73w34 mycobacteri
903	23	100.0	317	2	Q826F4	Q826f4 streptomyc	976	23	100.0	332	2	Q8D8K6	Q8d8k6 vibrio vuln
904	23	100.0	318	2	O86YC0	O86yc0 homo sapien	977	23	100.0	332	2	Q7ZLU7	Q7zlu7 human immun
905	23	100.0	318	2	Q7NET6	Q7net6 gloebacter	978	23	100.0	333	2	Q92XE5	Q92xe5 rhizobium m
906	23	100.0	319	1	TCB1_RABIT	Tcb1 rabbit	979	23	100.0	334	1	DUS2_SYNY3	Dus2 synechocyst
907	23	100.0	319	2	Q59553	Q59553 mycobacteri	980	23	100.0	334	1	SCRR_KLEPN	Scrr klebsiella

981 23 100.0 334 2 Q6PRD4
 982 23 100.0 334 2 Q6ZAR5
 983 23 100.0 335 1 HEMZ MYCAV
 984 23 100.0 335 2 Q8MXF3
 985 23 100.0 335 2 Q9XTU3
 986 23 100.0 335 2 Q88QX5
 987 23 100.0 335 2 Q9CNK2
 988 23 100.0 335 2 Q9KSJ0
 989 23 100.0 335 2 Q9RGU4
 990 23 100.0 335 2 Q9CX85
 991 23 100.0 335 2 Q98YGA
 992 23 100.0 336 2 Q8IXR7
 993 23 100.0 336 2 Q8WSM6
 994 23 100.0 336 2 Q7DSH6
 995 23 100.0 336 2 Q64WV9
 996 23 100.0 336 2 Q7U7E6
 997 23 100.0 336 2 Q89VM0
 998 23 100.0 336 2 Q8A3W7
 999 23 100.0 336 2 Q8CVB9
 1000 23 100.0 336 2 Q6GLH2

ALIGNMENTS

RESULT 1
 Q91HB7 PRELIMINARY; PRT; 30 AA.
 AC Q91HB7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ORF2 (Fragment).
 OS TT virus.
 OC Viruses; ssDNA viruses; Anellovirus.
 OX NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bagaglio S., Morsica G., Sitia G.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY035368; AAK77020.1; -
 FT NON TER 30 30
 SQ SEQUENCE 30 AA; 3180 MW; 87EF45FB63BF7D15 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 16 GQPR 19

RESULT 2
 Q8VJ21 PRELIMINARY; PRT; 31 AA.
 AC Q8VJ21;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=MT3449.2;
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RX MEDLINE=22206494; PubMed=12218036;
 RI DOI=10.1128/JB.184.19.5479-5490.2002;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,

RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
 RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
 RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
 RA Fraser C.M.;
 RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains.";
 RL J. Bacteriol. 184:5479-5490 (2002).
 DR EMBL; AF000516; AAK47793.1; -
 DR TIGR; MT3449.2; -
 KW Hypothetical protein.
 SQ SEQUENCE 31 AA; 3532 MW; 7AB847CE65D3449 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 11 GQPR 14

RESULT 3
 O06618 PRELIMINARY; PRT; 34 AA.
 AC O06618;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=Rv1572c;
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
 RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
 RA Tekala F., Badcock K., Basham D., Brown D., Chillingworth T.,
 RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
 RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
 RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence.";
 RL Nature 393:537-544 (1998).
 DR EMBL; BX842577; CAB09065.2; -
 DR Tuberculist; Rv1572c; -
 KW Complete proteome.
 SQ SEQUENCE 34 AA; 4005 MW; 2DCC9C17846AA537 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 9 GQPR 12

RESULT 4
 Q7TZW6 PRELIMINARY; PRT; 34 AA.
 AC Q7TZW6;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein Mb1598A.
 GN Name=Mb1598A; ORFNames=Mb1598A;
 OS Mycobacterium bovis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AF2122/97;
 RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
 RA Garnier T., Eiglmeyer K., Camus J.-C., Medina N., Mansoor H.,
 RA Pryor M., Eithov S., Grondin S., Lacroix C., Monsemp C., Simon S.,
 RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
 RA Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
 RT "The complete genome sequence of Mycobacterium bovis";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
 DR EMBL; BX248339; CAD96266.1;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 34 AA; 4005 MW; 2DC9C17846AA537 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 9 GQPR 12

RESULT 5
 Q679Y6 PRELIMINARY; PRT; 35 AA.
 AC Q679Y6;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Mitochondrial DNA polymerase (Fragment).
 GN Name=POLG;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rovic A.T., Jacobs H.T.;
 RT "PolyQ of POLG in Primates";
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AV376482; AAR26639.1;
 FT NON_TER 1 1
 35
 SQ SEQUENCE 35 AA; 4062 MW; DE8831E291285E4 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 30 GQPR 33

RESULT 6
 Q679Y8 PRELIMINARY; PRT; 36 AA.
 AC Q679Y8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Mitochondrial DNA polymerase (Fragment).
 GN Name=POLG;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Rovic A.T., Jacobs H.T.;
 RT "PolyQ of POLG in Primates";
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AV376480; AAR26637.1;
 FT NON_TER 1 1
 36
 SQ SEQUENCE 36 AA; 4219 MW; A82FEAD61CS86C3 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 31 GQPR 34

RESULT 7
 Q9UEU6 PRELIMINARY; PRT; 39 AA.
 AC Q9UEU6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Autosomal dominant polycystic kidney disease type II protein (Fragment).
 DE Homo sapiens (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96207227; PubMed=8619474; DOI=10.1006/abio.1996.0138;
 RA Andersson B., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.;
 RT "A 'double adaptor' method for improved shotgun library construction";
 RL Anal. Biochem. 236:107-113(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97264341; PubMed=9110174;
 RA Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
 RA Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
 RT "Large-scale concatenation cDNA sequencing";
 RL Genome Res. 7:353-358(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Yu W., Gibbs R.A.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF054992; AAC09351.1;
 FT NON_TER 1 1
 39
 SQ SEQUENCE 39 AA; 3837 MW; E4B4FE1DF07DIAD5 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 8 GQPR 11

RESULT 8
 IM9A RAT STANDARD; PRT; 43 AA.
 ID IM9A RAT
 AC Q9WV37;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Mitochondrial import inner membrane translocase subunit TIM9 A (Fragment).

GN Name=Timm9; Synonyms=Tim9a, Timm9a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RA Bauer M.P., Brunner M., Hofmann S.;
RT "Cloning and mapping of the Tim10/NDP gene family encoding small zinc
finger proteins involved in mitochondrial carrier import.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
similarity).
CC -!- SIMILARITY: Belongs to the Tim8/Tim10 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
DR EMBL; AF150102; AAD40008.1; ALT TERM.
KW Inner membrane; Mitochondrion; Protein transport; Translocation;
KW Transport.
FT NON-TER.
SQ SEQUENCE 43 AA; 5003 MW; 462223C352P4168A7 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 40 GQPR 43

RESULT 9
Q6WZF9
ID Q6WZF9 PRELIMINARY; PRT; 52 AA.
AC Q6WZF9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686J11229 (Fragment).
GN Name=DKFZp686J11229;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Human small intestine;
RC The German Human cDNA Consortium;
RG Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Robo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX647062; CAE46080.1; -.
KW Hypothetical protein.
FT NON-TER 52
SQ SEQUENCE 52 AA; 5516 MW; B67A9A9DDFDEBE25 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 38 GQPR 41

RESULT 10

Q71V32
ID Q71V32 PRELIMINARY; PRT; 59 AA.
AC Q71V32;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mevalonate pyrophosphate decarboxylase (Fragment).
GN Name=Mvpd;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato N., Ueno K., Sawamura M., Nabika T., Yamori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF036709; AAB92551.1; -.
FT NON-TER 1
FT NON-TER 59
SQ SEQUENCE 59 AA; 6674 MW; 8B6353329B34DDCF CRC64;

Query Match 100.0%; Score 23; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 13 GQPR 16

RESULT 11
Q54820
ID Q54820 PRELIMINARY; PRT; 61 AA.
AC Q54820;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Dnm protein.
GN Name=dnm;
OS Streptomyces peucetius.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1950;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97086506; PubMed=8932700;
RA Gallo M.A., Ward J., Hutchinson C.R.;
RT "The dnm gene in Streptomyces peucetius contains a naturally
RT occurring frameshift mutation that is suppressed by another locus
RT outside of the daunorubicin-production gene cluster.";
RL Microbiology 142:0-0(0).
DR EMBL; L47163; AAB50924.1; -.
SQ SEQUENCE 61 AA; 6572 MW; AD0A0E3DCE1F3F5A CRC64;

Query Match 100.0%; Score 23; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 45 GQPR 48

RESULT 12
Q6BWM8
ID Q6BWM8 PRELIMINARY; PRT; 62 AA.
AC Q6BWM8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Debaryomyces hansenii chromosome B of strain CBS767 of Debaryomyces
DE hansenii.
GN ORFNames=DEHA0B10318G;

Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	GQPR 4							
Db	9	GQPR 12							
RESULT 14									
Q8YMW9									
ID	Q8YMW9	PRELIMINARY;		PRT;		65	AA.		
AC	Q8YMW9;								
DT	01-MAR-2002	(TEMBLrel. 20, Created)							
DT	01-MAR-2002	(TEMBLrel. 20, Last sequence update)							
DT	01-JUN-2003	(TEMBLrel. 24, Last annotation update)							
DE	Asl4805 protein.								
GN	OrderedLocusNames=asl4805;								
OS	Anabaena sp. (strain PCC 7120).								
OC	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.								
OX	NCBI_TaxID=103690;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=21595285; PubMed=11759840;								
RA	Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,								
RA	Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,								
RA	Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,								
RA	Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,								
RA	Yasuda M., Tabata S.;								
RT	"Complete genomic sequence of the filamentous nitrogen-fixing								
RT	Cyanobacterium Anabaena sp. strain PCC 7120."								
RL	DNA Res. 8:205-213(2001).								
DR	EMBL; AP003597; BAB76504.1; -.								
DR	PIR; AE2406; AE2406.								
KW	Complete proteome.								
SQ	SEQUENCE 65 AA; 7215 MW; E37D308DA33AC44 CRC64;								
Query Match 100.0%; Score 23; DB 2; Length 65;									
Best Local Similarity 100.0%; Pred. No. 6.9e-02;									
Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	GQPR 4							
Db	27	GQPR 30							
RESULT 15									
Q9X880									
ID	Q9X880	PRELIMINARY;		PRT;		67	AA.		
AC	Q9X880;								
DT	01-OCT-2000	(TEMBLrel. 15, Created)							
DT	01-OCT-2000	(TEMBLrel. 15, Last sequence update)							
DT	01-MAR-2004	(TEMBLrel. 26, Last annotation update)							
DE	BH3126 protein.								
GN	OrderedLocusNames=BH3126;								
OS	Bacillus halodurans.								
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.								
OX	NCBI_TaxID=86665;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN-C-125;								
RX	MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;								
RA	Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,								
RA	Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,								
RA	Horikoshi K.;								
RT	"Complete genome sequence of the alkaliphilic bacterium Bacillus								
RT	halodurans and genomic sequence comparison with Bacillus subtilis."								
RL	Nucleic Acids Res. 28:4317-4331(2000).								
DR	EMBL; AP001517; BAB06845.1; -.								
DR	PIR; F84040; F84040.								
DR	GO; GO:0008151; P:cell growth and/or maintenance; IEA.								
DR	InterPro; IPR001455; SirA_like.								
KW	Complete proteome.								
SQ	SEQUENCE 67 AA; 7735 MW; 0825029A4C8FBC4E CRC64;								

Query Match 100.0%; Score 23; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 58 GQPR 61

RESULT 16

Q7UWU3 PRELIMINARY; PRT; 72 AA.
 AC Q7UWU3
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE Hypothetical protein.
 GN OrderedLocusNames=RB1787;
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Firellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Firellula sp.
 RT strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
 DR EMBL; BX294135; CAD72269.1; --
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 72 AA; 8185 MW; 21E56AE94AF1337C CRC64;

Query Match 100.0%; Score 23; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 47 GQPR 50

RESULT 17

Q7PFF50 PRELIMINARY; PRT; 73 AA.
 AC Q7PFF50
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE ENSANGP0000022726 (Fragment).
 GN Name=ENSANGG00000021610;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB01008807; EAA45464.1; --
 FT NON TER
 FT 1
 SQ SEQUENCE 73 AA; 7734 MW; 5DA167D728A8C629 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 46 GQPR 49

RESULT 18

Q6A863 PRELIMINARY; PRT; 73 AA.
 AC Q6A863
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=PPA1303;
 OS Propionibacterium acnes.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Propionibacteriaceae; Propionibacteriaceae; Propionibacterium.
 OX NCBI_TaxID=1747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KPA171202 / DSM 16379;
 RX PubMed=15286373; DOI=10.1126/science.1100330;
 RA Brueggemann H., Henne A., Hoster F., Liesegang H., Wierer A.,
 RA Strittmatter A., Hujer S., Duerre P., Gottschalk G.;
 RT "The complete genome sequence of Propionibacterium acnes, a commensal
 RT of human skin.";
 RL Science 305:671-673 (2004).
 DR EMBL; AB017283; AAT83052.1; --
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 73 AA; 7703 MW; 6BDAE2B358897DEE CRC64;

Query Match 100.0%; Score 23; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 52 GQPR 55

RESULT 19

Q80W36 PRELIMINARY; PRT; 73 AA.
 AC Q80W36
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b,
 DE isoform 1.
 GN Name=Atp5f1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=223988257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallah S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC049640; AAR49640.1; -.
DR MGD; MGI:1100495; Atp5f1.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR InterPro; IPR008688; Mt_ATP-synth_B.
DR Pfam; PF05405; Mt_ATP-synt_B; 1.
SQ SEQUENCE 73 AA; 7703 MW; 8D05D748E6292FBE CRC64;

Query Match 100.0%; Score 23; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 37 GQPR 40

RESULT 20
Q7V8P7 PRELIMINARY; PRT; 74 AA.
AC Q7V8P7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical.
GN OrderedLocusNames=PMW0288;
OS Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=74547;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR ENBL; BX572095; CAE20463.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 74 AA; 7920 MW; 37D987F91F33C9F1 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 55 GQPR 58

RESULT 21
Q8DH17 PRELIMINARY; PRT; 75 AA.
AC Q8DH17;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Tsl1972 protein.
GN OrderedLocusNames=tsl1972;

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OS Synechococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;
RX MEDLINE=22225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
DR ENBL; AP005375; BAC09524.1; -.
KW Complete proteome.
SQ SEQUENCE 75 AA; 8106 MW; 91EDBB412CEE1B1C CRC64;

Query Match 100.0%; Score 23; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 27 GQPR 30

RESULT 22
Q6TLY2 PRELIMINARY; PRT; 76 AA.
AC Q6TLY2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ketosynthase (Fragment).
OS Streptomyces hygroscopicus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1912;
RN [1]
RP SEQUENCE FROM N.A.
RA Ayuso A., Genilloud O.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY394458; AAR01271.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR000794; Ketoacyl-synth.
DR Pfam; PF02801; Ketoacyl-synt_C; 1.
DR NON_TER 1
FT NON_TER 76
SQ SEQUENCE 76 AA; 7978 MW; B4593E57C280E8BF CRC64;

Query Match 100.0%; Score 23; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 61 GQPR 64

RESULT 23
Q7R5L8 PRELIMINARY; PRT; 77 AA.
AC Q7R5L8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GUP_487_7109570862.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RA "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000004; EAA42624.1; -.
SQ SEQUENCE 77 AA; 8263 MW; ADAF8BC487DC40AD CRC64;

Query Match 100.0%; Score 23; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 51 GQPR 54

RESULT 24
Q6ESF6 PRELIMINARY; PRT; 81 AA.
ID Q6ESF6;
AC Q6ESF6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein P0605D08.19.
GN Names=P0605D08.19;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005110; BAD28414.1; -.
KW Hypothetical protein.
SQ SEQUENCE 81 AA; 8367 MW; 7AFC9E7C4992B349 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 77 GQPR 80

RESULT 25
Q8P835 PRELIMINARY; PRT; 81 AA.
ID Q8P835;
AC Q8P835;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 25, Last annotation update)
DE Sarcosine oxidase alpha subunit.
GN Names=soxa; OrderedLocusNames=XCC2413;
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P.,

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RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorty H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AS012352; AAM41691.1; -.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001041; Ferredoxin.
KW Complete proteome.
SQ SEQUENCE 81 AA; 8559 MW; 0A68118C1BBA718D CRC64;

Query Match 100.0%; Score 23; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 39 GQPR 42

RESULT 26
Q72CR2 PRELIMINARY; PRT; 81 AA.
ID Q72CR2;
AC Q72CR2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=DVU1221;
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS 8303).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15077118; DOI=10.1038/nbt959;
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA Peterson J.D., Davidesen T.M., Zafar N., Zhou L., Radune D.,
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT Desulfovibrio vulgaris Hildenborough.";
RL Nat. Biotechnol. 22:554-559(2004).
DR EMBL; AS017313; AAS95699.1; -.
DR TIGR; DVU1221; -.
KW Complete proteome.
SQ SEQUENCE 81 AA; 8857 MW; 964517E2E58D9E54 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 31 GQPR 34

RESULT 27
Q96Q33

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ID Q96Q33 PRELIMINARY; PRT; 82 AA.
AC Q96Q33;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ALS2CR14 protein.
GN Name=ALS2CR14;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21470351; PubMed=11586298; DOI=10.1038/ngl001-166;
RA Hadano S., Hand C.K., Osuga H., Yanagisawa Y., Otsu A., Devon R.S.,
RA Miyamoto N., Showguchi-Miyata J., Okada Y., Singaraja R.,
RA Figlewicz D.A., Kwiatkowski T., Hosler B.A., Sagie T., Skaug J.,
RA Nasir J., Brown R.H., Jr, Scherer S.W., Rouleau G.A., Hayden M.R.,
RA Ikeda J.-E.;
RT "A gene encoding a novel GTPase regulator is mutated in familial
RT amyotrophic lateral sclerosis 2.";
RL Nat. Genet. 29:166-173(2001).
DR EMBL; AB053316; BAB9024.1; -.
DR Genew; HGNC:14441; ALS2CR14.
DR InterPro; IPR010504; Arfaptin.
DR Pfam; PF06456; Arfaptin; 1.
DR PROSITE; PS00870; AH; 1.
SQ SEQUENCE 82 AA; 9599 MW; 77B0D7E497517FEF CRC64;

Query Match 100.0%; Score 23; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db |||||
5 GQPR 8

RESULT 28
Q9X5W4 PRELIMINARY; PRT; 82 AA.
AC Q9X5W4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MoaD.
GN Name=moaD;
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=37b4;
RA Solomon P.S., Shaw A.L., McEwan A.G.;
RA Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF128444; AAD21202.1; -.
DR HSP; P30748; IJW9.
DR GO; GO:0006790; P:sulfur metabolism; IEA.
DR InterPro; IPR010034; MoaD.
DR InterPro; IPR003749; ThisS.
DR Pfam; PF02597; ThisS; 1.
DR TIGRFAMs; TIGR01682; moaD; 1.
SQ SEQUENCE 82 AA; 8895 MW; A97135C7BCC2AA17 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db |||||
15 GQPR 18

RESULT 29
Q86TT0 PRELIMINARY; PRT; 85 AA.
AC Q86TT0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Full-length cDNA clone CS0DC020YCl2 of Neuroblastoma of Homo sapiens
DE (human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Neuroblastoma;
RA Li W.B., Gruber C., Jesse J., Polayes D.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Neuroblastoma;
RA Genoscope;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX161407; CAD61886.1; -.
SQ SEQUENCE 85 AA; 9314 MW; BD506B062C499167 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db |||||
58 GQPR 61

RESULT 30
Q8S0W2 PRELIMINARY; PRT; 85 AA.
AC Q8S0W2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE QJ1014_G12.12 protein.
GN Name=QJ1014_G12.12;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayaishi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Ikonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabu Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakaishima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AF003372; BAB89078.1; -.
DR Gramene; Q8S0W2; -.
SQ SEQUENCE 85 AA; 9060 MW; 6B20E85090EFAE3F CRC64;

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Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 16 GQPR 19

RESULT 31
Q856X1
ID Q856X1 PRELIMINARY; PRT; 86 AA.
AC Q856X1;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Gp63.
OS Mycobacteriophage Rosebush.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=205874;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;
RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
RA Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA Hatfull G.F.;
RT "Origins of highly mosaic mycobacteriophage genomes.";
RL Cell 113:171-182(2003).
DR EMBL; AY129334; ANA01905.1; -
SQ SEQUENCE 86 AA; 9533 MW; 6E7BB1F300737C5C CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 86;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 6 GQPR 9

RESULT 32
Q8WZ93
ID Q8WZ93 PRELIMINARY; PRT; 87 AA.
AC Q8WZ93;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE NAG11.
GN Name=NAG11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nasopharyngeal epithelium;
RA Yu Y., Li G.Y.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170307; AAL35407.1; -
SQ SEQUENCE 87 AA; 9840 MW; 5EDA46F2A7D6524E CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 53 GQPR 56

RESULT 33
Q7U442
ID Q7U442 PRELIMINARY; PRT; 87 AA.
AC Q7U442;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein precursor.
GN OrderedLocusNames=SYNW2233;
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
RA Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J.,
RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus.";
RL Nature 424:1037-1042(2003).
DR EMBL; BX569695; CAE08748.1; -
KW Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 69 87 Potential.
SQ SEQUENCE 87 AA; 9597 MW; 9E9CE/ACCB35960B CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Length 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 39 GQPR 42

RESULT 34
GVPB_BACME
ID GVPB_BACME STANDARD; PRT; 88 AA.
AC G68677;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Gas vesicle structural protein B (GVP B).
GN Name=gvpB;
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VT1660;
RX MEDLINE=98233742; PubMed=9573198;
RA Li N., Cannon M.C.;
RT "Gas vesicle genes identified in Bacillus megaterium and functional expression in Escherichia coli.";
RL J. Bacteriol. 180:2450-2458(1998).
CC -I- FUNCTION: Gas vesicles are small, hollow, gas filled protein structures that are found in several microbial planktonic microorganisms. They allow the positioning of the organism at the favorable depth for growth. GvpA type proteins form the essential core of the structure.
CC -I- SUBCELLULAR LOCATION: Gas vesicle membrane.
CC -I- SIMILARITY: Belongs to the gas vesicle protein type A family.
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CC -----
CC EMBL; AF053765; AAC38416.1; -
CC HAMAP; MF00576; -; 1.
CC InterPro; IPR000638; Gas_vesicle.
CC Pfam; PF00741; Gas_vesicle; 1.
CC -----
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DR ProDom; PD003598; Gas_vesicle; 1.
DR PROSITE; PS00234; GAS_VESICLE_A.1; 1.
DR PROSITE; PS00669; GAS_VESICLE_A.2; 1.
KW Gas vesicle.
SQ SEQUENCE 88 AA; 9618 MW; 5F089DE77358D84A CRC64;

Query Match 100.0%; Score 23; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. NO. 9.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 82 GQPR 85

RESULT 35
IM9A_HUMAN
ID IM9A_HUMAN STANDARD; PRT; 89 AA.
AC Q9Y5J7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Mitochondrial import inner membrane translocase subunit TIM9 A.
GN Names=TIM9; Synonyms=Tim9A, TIM9A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20021763; PubMed=10552927; DOI=10.1006/geno.1999.5966;
RA Jin H., Kendall E., Freeman T.C., Roberts R.G., Vetrle D.L.;
RT "The human family of deafness/dystonia peptide (DDP) related
RL mitochondrial import proteins.";
RN Genomics 61:259-267(1999).
[2]
SEQUENCE FROM N.A.
RP Bauer M.F., Brunner M., Hofmann S.;
RT "Cloning and mapping of the Tim10/DDP gene family encoding small zinc
RL finger proteins involved in mitochondrial carrier import.";
RN Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RP TISSUE=Placenta, and Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Likely to be involved in the import and insertion of
CC hydrophobic membrane proteins into the mitochondrial inner
CC membrane.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
CC similarity).
CC -!- TISSUE SPECIFICITY: Ubiquitous, with highest expression in heart,
CC kidney, liver and skeletal muscle.
CC -!- SIMILARITY: Belongs to the Tim8/Tim10 family.

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CC -----
CC EMBL; AF152353; AAF15103.1; -
CC EMBL; AF150100; AAD40006.1; -
CC EMBL; BC020213; AAH20213.1; -
CC EMBL; BC054875; AAH54875.1; -
CC PIR; T51191; T51191.
CC Genew; HGNC:11819; TIMM9.
CC MIM; 607384; -
CC GO; GO:0005744; C-mitochondrial inner membrane presequence tr. . .; TAS.
CC GO; GO:0008270; F-zinc ion binding; TAS.
CC GO; GO:0007605; P-protein-mitochondrial targeting; TAS.
CC GO; GO:0006626; P-protein-mitochondrial targeting; TAS.
CC InterPro; IPR004217; Znf.Tim10/DDP.
CC Pfam; PF02953; zf-Tim10/DDP.
CC Inner membrane; Mitochondrion; Protein transport; Translocation;
KW Transport.
SQ SEQUENCE 89 AA; 10378 MW; 00F17CF6332ABF48 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 89;
Best Local Similarity 100.0%; Pred. NO. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 86 GQPR 89

RESULT 36
IM9A_MOUSE
ID IM9A_MOUSE STANDARD; PRT; 89 AA.
AC Q9WV98;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Mitochondrial import inner membrane translocase subunit TIM9 A.
GN Names=Tim9; Synonyms=Tim9a, Timm9a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP Bauer M.F., Brunner M., Hofmann S.;
RT "Cloning and mapping of the Tim10/DDP gene family encoding small zinc
RL finger proteins involved in mitochondrial carrier import.";
RN Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimm S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Naglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagahima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

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RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume M., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane (By
CC similarity).
CC -1- SIMILARITY: Belongs to the Tim8/Tim10 family.
CC -----
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CC -----
DR EMBL; AF150101; AAD40007.1; -.
DR EMBL; AK018764; BAB31394.1; -.
DR EMBL; BC024370; AAH24370.1; -.
DR PIR; T51192; T51192.
DR MGD; MGI:1353432; Timm9.
DR InterPro; IPR004217; Znf_Tim10/DDP.
DR Pfam; PF02953; znf-Tim10/DDP; 1.
KW Inner membrane; Mitochondrion; Protein transport; Translocation;
KW Transport.
SQ SEQUENCE 89 AA; 10344 MW; 1A40D7F491A09548 CRC64;
Query Match 100.0%; Score 23; DB 1; Length 89;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 86 GQPR 89
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RESULT 37
Q68V99 PRELIMINARY; PRT; 89 AA.
ID Q68V99
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AC Q68V99;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative methane monooxygenase, alpha subunit (fragment).
GN Name=pmoA;
OS uncultured methanotrophic bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=288814;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolb S., Knief C., Dunfield P., Conrad R.;
RT "Abundance and activity of uncultured methanotrophic bacteria involved
RT in consumption of atmospheric methane in two forest soils.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ786669; CAH10419.1; -.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR InterPro; IPR005829; Sug transporter.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
KW Monooxygenase.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 9839 MW; 8A70CB602A043513 CRC64;
Query Match 100.0%; Score 23; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 7 GQPR 10
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RESULT 38
Q9DSU8 PRELIMINARY; PRT; 89 AA.
ID AC Q9DSU8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Ascovirus DpAV4.
OC Viruses; dsDNA viruses, no RNA stage; Ascoviridae; Ascovirus.
OX NCBI_TaxID=113365;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20540044; PubMed=11086137;
RA Stasiak K., Demattai M.V., Federici B.A., Bigot Y.;
RT "Phylogenetic position of the Diadromus pulchellus ascovirus DNA
RT polymerase among viruses with large double-stranded DNA genomes.";
RL J. Gen. Virol. 81:3059-3072 (2000).
DR EMBL; AJ279813; CAC19137.1; -.
DR InterPro; IPR003439; ABC transporter.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 89 AA; 9743 MW; E8FEF817BCF22BCE CRC64;
Query Match 100.0%; Score 23; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 27 GQPR 30
|||||
RESULT 39
HYPC_ECOLI STANDARD; PRT; 90 AA.
ID HYPC_ECOLI
AC F24191;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
```


DE Hydrogenase isoenzymes formation protein hypc.
GN Name=hypC;
GN OrderedLocusNames=b2728, c3288, z4037, ECs3584, SF2745, S2937;
OS Escherichia coli, O6,
OS Escherichia coli O157:H7, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992, 83334, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RA MEDLINE=91194542; PubMed=1849603;
RA Lutz S., Jacobi A., Schlensog V., Boehm R., Sawers G., Boeck A.;
RT "Molecular characterization of an operon (hyp) necessary for the
RT activity of the three hydrogenase isoenzymes in Escherichia coli.";
RL Mol. Microbiol. 5:123-135(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RA MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=11206551; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/IAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
RN [9]
RP POSSIBLE FUNCTION.
RC SPECIES=E.coli;
RX MEDLINE=98153119; PubMed=9485446; DOI=10.1021/bi9720078;
RA Drapal N., Boeck A.;
RT "Interaction of the hydrogenase accessory protein HypC with HycE, the
RT large subunit of Escherichia coli hydrogenase 3 during enzyme
RT maturation.";
RL Biochemistry 37:2941-2948(1998).
CC -!- FUNCTION: Is required for the formation of all three hydrogenase
CC isoenzymes. May bind to the precursor form of the large subunit of
CC dehydrogenases to keep them in a conformation accessible for metal
CC incorporation.
CC -!- SIMILARITY: Belongs to the hypF/hypC family.
CC
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CC EMBL; X54543; CAA38414.1; -;
CC EMBL; U29579; AAA69238.1; -;
CC EMBL; U00096; AAC75770.1; -;
CC EMBL; AE016765; AAN81737.1; -;
CC EMBL; AE005501; AAG57836.1; -;
CC EMBL; AP002562; BAB37007.1; -;
CC EMBL; AE015289; AAN44236.1; -;
CC EMBL; AE016987; AAP18063.1; -;
CC PIR; H85921; H85921.
CC PIR; H91076; H91076.
CC PIR; S15199; S15199.
CC ECO2DBASE; A008.0; 6TH EDITION.
CC ECHOBASE; EB0480; -;
CC EcoGene; EG10485; hypC.
CC InterPro; IPR001109; HypF_HypC.
CC InterPro; IPR008994; Nucleic_acid_OB.
CC Pfam; PF01455; HypF_HypC; 1.
CC PIRSF; PIRSF005618; HypF_HypC; 1.
CC PRINTS; PR00445; HUPFHYP.
CC PRODOM; PD003112; HypF_HypC; 1.
CC TIGRFAMs; TIGR00074; hypC_hupF; 1.
CC PROSITE; PS01097; HUPF_HYP; 1.
CC Complete proteome.
SQ SEQUENCE 90 AA; 9732 MW; FBE252F1875C7879 CRC64;
Query Match 100.0%; Score 23; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY : 1 GQPR 4
Db 40 GQPR 43
RESULT 40
Q8XG01 PRELIMINARY; PPT; 90 AA.
ID Q8XG01

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AC Q8XG01; Q7AMES;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hydrogenase isoenzymes formation protein hupC.
GN Name=hupC; OrderedLocusNames=STV2978, t2758;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=21534947; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyfanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feitwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AE016843; AA070319.1; -.
DR ENBL; AL627276; CAD05963.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR PFam; PF01455; HupF_HyPC; 1.
DR PIRSF; PIRSF005618; HupF_HyPC; 1.
DR PRINTS; PR00445; HUPFHYP.
DR PRODom; PD003112; HupF_HyPC; 1.
DR TIGRFAMs; TIGR00074; hupC_hupF; 1.
DR PROSITE; PS01097; HUPF_HYPC; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 90 AA; 9744 MW; 6D1F99EB36EC6555 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 40 GQPR 43

RESULT 41
Q7CFX9 PRELIMINARY; PRT; 90 AA.
ID Q7CFX9
AC Q7CFX9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative hydrogenase expression/formation protein.
GN Name=hupC; OrderedLocusNames=STW2856;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;

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RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
DR EMBL; AS008830; AAL21736.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001109; HupF_HyPC.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR PFam; PF01455; HupF_HyPC; 1.
DR PIRSF; PIRSF005618; HupF_HyPC; 1.
DR PRINTS; PR00445; HUPFHYP.
DR PRODom; PD003112; HupF_HyPC; 1.
DR TIGRFAMs; TIGR00074; hupC_hupF; 1.
DR PROSITE; PS01097; HUPF_HYPC; 1.
KW Complete proteome.
SQ SEQUENCE 90 AA; 9744 MW; 6D1F99EB36EC6555 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 40 GQPR 43

RESULT 42
Q7W0F6 PRELIMINARY; PRT; 90 AA.
ID Q7W0F6
AC Q7W0F6
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative exported protein.
GN OrderedLocusNames=BP0181;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tohama I. / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12310271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feitwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch B., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640411; CAE40560.1; -.
KW Complete proteome.
SQ SEQUENCE 90 AA; 9780 MW; 30CA43B5FD67A8B3 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 75 GQPR 78

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RESULT 43
Q7W1D7 PRELIMINARY; PRT; 90 AA.
AC Q7W1D7;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Putative exported protein.
GN OrderedLocusNames=BPP0756;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cardeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640425; CAB40165.1; -.
KW Complete proteome.
SQ SEQUENCE 90 AA; 9812 MW; 30DE13B5FD67A8B3 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 75 GQPR 78

RESULT 44
Q7WP44 PRELIMINARY; PRT; 90 AA.
AC Q7WP44;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Putative exported protein.
GN OrderedLocusNames=BB0841;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cardeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).

Query Match 100.0%; Score 23; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 75 GQPR 78

RESULT 45
Q8YZR28 PRELIMINARY; PRT; 91 AA.
AC Q8YZR28;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Aar3294 protein.
GN OrderedLocusNames=aar3294;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Iehikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003592; BAB74993.1; -.
DR PIR; AG2217; AG2217.
DR GO; GO:0006790; P:sulfur metabolism; IEA.
DR Pfam; PF02597; This; 1.
KW Complete proteome.
SQ SEQUENCE 91 AA; 9679 MW; 93965078BD48EEF CRC64;

Query Match 100.0%; Score 23; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 51 GQPR 54

RESULT 46
Q84VP6 PRELIMINARY; PRT; 92 AA.
AC Q84VP6;
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Hypothetical protein At5g21110.
GN Names=At5g21110;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Town C.D., Haas B.J., Maiti R., Hannick L.I., Chan A.P., Ronning C.M.,
RA Smith Jr R.K., Arbogast T., Tallon L.J., Utterback T.R., VanAken S.E.,
RA Feldblum T.V., Yu C., Wortman J.R., White O., Fraser C.M.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC140977; AAC073885.1; -.

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KW Hypothetical protein.
SQ SEQUENCE 92 AA; 10268 MW; 9229E7FCBEFF144F CRC64;

Query Match 100.0%; Score 23; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 14 GQPR 17

RESULT 47
Q91UP6 PRELIMINARY; PRT; 94 AA.
AC Q91UP6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Plasmid pSB102.
OG Plasmid pSB102.
OC other sequences; broad host range plasmids.
OX NCBI_TaxID=146518;
RN [1]
RA Schneiker S., Keller M., Droegge M., Lanka E., Puehler A.,
RA selbitschka W.;
RT "The genetic organization and evolution of the broad-host-range
RT mercury resistance plasmid pSB102 isolated from a microbial population
RT residing in the rhizosphere of alfalfa.";
RL Nucleic Acids Res. 29:5169-5181(2001).
DR EMBL: AJ304453; CAC79191.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 94 AA; 10338 MW; 3DB2F5265FF12C84 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 50 GQPR 53

RESULT 48
Q8SA29 PRELIMINARY; PRT; 95 AA.
AC Q8SA29;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE P0684E06.15 protein (P0445H04.6 protein).
GN Names=P0684E06.15; Synonyms=P0445H04.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
SQ SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Negamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakana Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,

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RA Waki K., Yamagata H., Yamane H., Yoshiaki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL: AF003291; BAB85269.1; -.
DR EMBL: AF004364; BAC06295.1; -.
DR Gramene; Q8SA29; -.
SQ SEQUENCE 95 AA; 10364 MW; 92507AEF0533E2F0 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 16 GQPR 19

RESULT 49
Q9F6C4 PRELIMINARY; PRT; 96 AA.
AC Q9F6C4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Propionicin Tl.
GN Name=pctA;
OS Propionibacterium thoenii.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Propionibacteriaceae; Propionibacteriaceae; Propionibacterium.
OX NCBI_TaxID=1751;
RN [1]
SQ SEQUENCE FROM N.A.
RX MEDLINE=20466828; PubMed=11010864;
RX DOI=10.1128/AEM.66.10.4230-4236.2000;
RA Faye T., Langsrud T., Nes I.F., Holo H.;
RT "Biochemical and genetic characterization of propionicin Tl, a new
RT bacteriocin from Propionibacterium thoenii.";
RL Appl. Environ. Microbiol. 66:4230-4236(2000).
DR EMBL: AF294258; AAG24829.1; -.
SQ SEQUENCE 96 AA; 10045 MW; ED11F314D1C78F8 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 86 GQPR 89

RESULT 50
Q9YCI1 PRELIMINARY; PRT; 98 AA.
AC Q9YCI1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein APES047.
GN ORFNames=APES047;
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
SQ SEQUENCE FROM N.A.
RX MEDLINE=93310339; PubMed=10382966;
RA Kwarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,

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RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6: 83-101(1999).
 DR ENBL; AP000061; BAA80266.1; -.
 DR PIR; D72601; D72601.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 98 AA; 10497 MW; C135B70F14DCC00B CRC64;

Query Match 100.0%; Score 23; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 DB 25 GQPR 28

RESULT 51

Q7QUD9 PRELIMINARY; PRT; 98 AA.
 AC Q7QUD9;
 DT 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE GLP 59 26262 25966.
 OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
 OX NCBI_TaxID=184922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.; Giardia lamblia genome.";
 RT "Draft sequence of the Giardia lamblia genome.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR ENBL; AACB0100094; EAA38654.1; -.
 SQ SEQUENCE 98 AA; 10946 MW; DB918E4612BB26D1 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 DB 45 GQPR 48

RESULT 52

Q68QC8 PRELIMINARY; PRT; 99 AA.
 AC Q68QC8;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Protease (Fragment).
 GN Name=pol;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rodrigues R., Custodio R.M., Ferreira J.L.P., Oliveira C.M.,
 RA Franco H.M., Ferreira L.S.B., Brigido L.F.M.;
 RT "ARV Resistance Mutations in Non-B clades HIV-1";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AY643155; AAR96726.1; -.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR InterPro; IPR001995; Peptidase_A2.

DR InterPro; IPR009007; Pept_Aspartic.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR Pfam; PF00077; RVP; 1.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
 KW Protease.
 FT NON_TER 1
 FT NON_TER 99
 SQ SEQUENCE 99 AA; 10715 MW; 8E209C85F9271B20 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 DB 17 GQPR 20

RESULT 53

Q9Q2H7 PRELIMINARY; PRT; 99 AA.
 AC Q9Q2H7;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE V-1 protease (Fragment).
 GN Name=ORF;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21091889; PubMed=11181376;
 RA Servais J., Lambert C., Fontaine E., Plessier J.M., Robert I.,
 RA Arendt V., Staub T., Schneider F., Hemmer R., Burtonboy G.,
 RA Schmit J.C.;
 RT "Variant human immunodeficiency virus type 1 proteases and response to
 RT combination therapy including a protease inhibitor.";
 RL Antimicrob. Agents Chemother. 45:893-900(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21102417; PubMed=11158089;
 RA Servais J., Lambert C., Fontaine E., Plessier J.M., Robert I.,
 RA Arendt V., Staub T., Schneider F., Hemmer R., Burtonboy G.,
 RA Schmit J.C.;
 RT "Comparison of DNA sequencing and a line probe assay for detection of
 RT human immunodeficiency virus Type 1 in patients failing highly active
 RT antiretroviral therapy.";
 RL J. Clin. Microbiol. 39:454-459(2001).
 RN [3]
 RP SEQUENCE FROM N.A.

RA Servais J.A.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ279595; CAB66008.1; -.
 DR GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001995; Peptidase A2.
 DR InterPro; IPR009007; Pept_Aspartic.
 DR Pfam; PF00077; RVP; 1.
 DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
 KW Protease.
 FT NON_TER 1
 FT NON_TER 99
 SQ SEQUENCE 99 AA; 10829 MW; 6DCA719E7FC94B1B CRC64;

Query Match 100.0%; Score 23; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||

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Db 17 GQPR 20
RESULT 54
Q90DC9 PRELIMINARY; PRT; 100 AA.
AC Q90DC9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Vpr protein.
GN Names=vpr;
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SIVsmSL92b;
RX MEDLINE=96211494; PubMed=8648696;
RA Chen Z., Telfier P., Gettie A., Read P., Zhang L., Ho D.D., Marx P.A.;
RT "Genetic characterization of new West African simian immunodeficiency
RT virus SIVsm: Geographic clustering of household-derived SIV strains
RT with human immunodeficiency virus type 2 subtypes and genetically
RT diverse viruses from a single feral sooty mangabey troop.";
RL J. Virol. 70:3617-3627(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SIVsmSL92b;
RX MEDLINE=21413368; PubMed=11522185; DOI=10.1089/089922201316912763;
RA Chakrabarti L.A., Luckay A., Marx P.A.;
RT "A divergent simian immunodeficiency virus from sooty mangabey with an
RT atypical Tat-TAR structure.";
RL AIDS Res. Hum. Retroviruses 17:1155-1165(2001).
DR EMBL; AF34679; AAK55278.1; -.
DR HSSP; P12520; 1BDE.
DR PFAM; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVVPRVPX.
KW AIDS.
SQ SEQUENCE 100 AA; 11433 MW; A420DE62297D7C8B CRC64;

Query Match 100.0%; Score 23; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 82 GQPR 85

-RESULT 55
Q7PJ39 PRELIMINARY; PRT; 101 AA.
AC Q7PJ39;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000024894.
GN Name=ENSANGG00000009298;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008964; EAA43910.1; -.
SQ SEQUENCE 101 AA; 11333 MW; CE6533E507EBE1E8 CRC64;
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Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 40 GQPR 43

RESULT 56
Q7G4Y8 PRELIMINARY; PRT; 101 AA.
AC Q7G4Y8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN ORFNames=OSJNB0011A24.34;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017063; AAP52397.1; -.
KW Hypothetical protein.
SQ SEQUENCE 101 AA; 10958 MW; DA57AD537DBC6603 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 36 GQPR 39

RESULT 57
Q88Q57 PRELIMINARY; PRT; 101 AA.
AC Q88Q57;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=PP0641;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.;
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzaz A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Fimmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
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RL Environ. Microbiol. 4:799-808 (2002).
DR EMBL; AF016776; AAN66266.1; -.
DR TIGR; PP0641; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 101 AA; 11214 MW; AC09CL37CE55B2D9 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db |||||
10 GQPR 13

RESULT 58
Q9RWS5 PRELIMINARY; PRT; 101 AA.
AC Q9RWS5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein DR0550.
GN OrderedLocusNames=DR0550;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.P., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamatheva J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577 (1999).
DR EMBL; AE001917; AAF10172.1; -.
DR PIR; F75500; F75500.
DR TIGR; DR0590; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 101 AA; 10629 MW; 74B390E0E8A827DC CRC64;

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db |||||
54 GQPR 57

RESULT 59
Q8UEN1 PRELIMINARY; PRT; 101 AA.
AC Q8UEN1; Q7CVN7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein Atu1725 (AGR_C_3166p).
GN OrderedLocusNames=AGR_C_3166, Atu1725;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dupont;

us-10-731-921-3.rup
MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley P., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Cereon;
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlet K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328 (2001).
DR EMBL; AE009129; AAL42724.1; -.
DR EMBL; AE008094; AAK87496.1; -.
DR PIR; AF2788; AF2788.
DR PIR; G97567; G97567.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 101 AA; 11070 MW; 6E5BB7180682BFC1 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db |||||
45 GQPR 48

RESULT 60
Q79F64 PRELIMINARY; PRT; 102 AA.
AC Q79F64;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE RNA-binding protein.
GN Name=rbpA1;
OS Anabaena variabilis.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=1172;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M3;
RX MEDLINE=94250845; PubMed=8193307;
RA Sato N.;
RT "A cold-regulated cyanobacterial gene cluster encodes RNA-binding
RT protein and ribosomal protein S21.";
RL Plant Mol. Biol. 24:819-823 (1994).
DR EMBL; D17710; BAA04563.1; -.
DR InterPro; IPR00504; RNA_rec_mot.
DR Pfam; PF00076; RRM 1; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 102 AA; 10963 MW; BA565080DB222875 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPCR 4
Db 39 QPCR 42

RESULT 61
Q44560 PRELIMINARY; PRT; 102 AA.
AC Q44560;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RNA-binding protein.
GN Name=rbpA1; OrderedLocNames=alr0741;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003583; BAB72698.1; -
DR PIR; AC1899; AC1899.
DR PIR; I39621; I39621.
DR HSP; P19339; 3SXL.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; RRM_1; 1.
DR SMART; SM00360; RRM_1.
DR PROSITE; PS0102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
KW Complete proteome.
SQ SEQUENCE 102 AA; 10963 MW; BA565080DB222875 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPCR 4
Db 39 QPCR 42

RESULT 62
Q8CAG4 PRELIMINARY; PRT; 102 AA.
ID Q8CAG4
AC Q8CAG4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched
DE library, clone:A230065N10 product:hypothetical protein, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chordonia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=39279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RC The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishida T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-Format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RW EMBL; AK038819; BAC30137.1; -
KW Hypothetical protein.
SQ SEQUENCE 102 AA; 10304 MW; BA9B3985529AEEF7 CRC64;

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Query Match 100.0%; Score 23; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPCR 4
Db 47 QPCR 50

RESULT 63
Q6Z289 PRELIMINARY; PRT; 103 AA.
ID Q6Z289
AC Q6Z289;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OSUNBa0086F04.21.

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GN Name=OSUNB0086F04.21;
OS Oryza sativa (japonica cultivar-group);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AP005388; BAC98679.1; -.
KW Hypochemical protein.
SQ SEQUENCE 103 AA; 11794 MW; 63F6CAD6D324CA2B CRC64;

Query Match 100.0%; Score 23; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 82 GQPR 85

RESULT 64
Q934X9 PRELIMINARY; PRT; 103 AA.
AC Q934X9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypochemical protein HCM2.0088c.
GN OrderedLocusNames=HCM2.0088c;
OS Salmonella typhi.
OG Plasmid pHCM2.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR ENBL; ALU53384; CAD09955.1; -.
KW Complete proteome; Hypochemical protein; Plasmid.
SQ SEQUENCE 103 AA; 11459 MW; 069BE3BE3A8B3324 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 12 GQPR 15

RESULT 65
Q6LV85 PRELIMINARY; PRT; 103 AA.
AC Q6LV85
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypochemical anti-anti-sigma regulatory factor.

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GN Name=VP1476; OrderedLocusNames=PBPR0351;
OS Photobacterium profundum (Photobacterium sp. (strain S89)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the anti-sigma-factor antagonist family.
CC -!- SIMILARITY: Contains 1 STAS domain.
DR ENBL; CR378664; CAG18790.1; -.
DR InterPro; IPR003658; Antisig_antgnst.
DR InterPro; IPR002645; STAS.
DR ProDom; PD005210; Antisig_antgnst; 1.
DR TIGRFAMs; TIGR00377; ant_ant_sig; 1.
DR PROSITE; PS50801; STAS; 1.
KW Complete proteome.
SQ SEQUENCE 103 AA; 11711 MW; 1CC19599E8E5D0EC CRC64;

Query Match 100.0%; Score 23; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 79 GQPR 82

RESULT 66
Q9Q2P0 PRELIMINARY; PRT; 103 AA.
AC Q9Q2P0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE RPS1 protein.
GN Names=rps1; Synonyms=RPMS1;
OS Human herpesvirus 4 (Epstein-Barr virus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10376;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C15;
RX MEDLINE=20173697; PubMed=10708423;
DOI=10.1128/JVI.74.7.3082-3092.2000;
RA Smith P.R., de Jesus O.D., Turner D., Hollyoake M.,
RA Elgueta Karstegi C., Griffin B.E., Karran L., Wang Y., Hayward D.,
RA Farrell P.J.;
RT "Structure and coding content of CST (BART) family RNAs of Epstein-
RT Barr virus.";
RL J. Virol. 74:3082-3092(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=84270667; PubMed=6087149;
DOI=10.1128/JVI.74.7.3082-3092.2000;
RA Baer R.J., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G.F., Hudson G.S., Satchwell S.C., Sequin C.,
RA Tuffnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=88283646; PubMed=2840285;
DOI=10.1128/JVI.74.7.3082-3092.2000;
RA Laux G., Perricaudet M., Farrell P.J.;
RT "A spliced Epstein-Barr virus gene expressed in immortalized
RT lymphocytes is created by circularization of the linear viral

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Db          37 GQPR 40
RESULT 67
VPR_HV2ST
ID_VPR_HV2ST STANDARD; PRT; 104 AA.
AC P20884;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE VPR protein (R ORF protein).
GN Name=VPR;
OS Human immunodeficiency virus type 2 (isolate ST) (HIV-2).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11721;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90112662; PubMed=2296086;
RA Kumar P., Hui H., Kappes J.C., Haggarty B.S., Hoxie J.A., Arya S.K.,
RA Shaw G.M., Hahn B.H.;
RT "Molecular characterization of an attenuated human immunodeficiency
RT virus type 2 isolate.";
RL J. Virol. 64:890-901(1990).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J04498; AAB00749.1; -
DR HSSP; P12520; IDSK
DR HIV; J04498; VPR$21SY.
DR InterPro; IPR000012; Retrov_Vpr/X.
DR Pfam; PF00522; VPR; 1.
DR PRINTS; PR00444; HIVPRVPX.
KW AIDS.
SQ SEQUENCE 105 AA; 11975 MW; 3E17584B2DOCC64F CRC64;

Query Match 100.0%; Score 23; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GQPR 4
Db          87 GQPR 90

RESULT 69
Q9FTT2
ID_Q9FTT2 PRELIMINARY; PRT; 106 AA.
AC Q9FTT2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE OSJNBa0086P08.25 protein (OSJNBa0010K01.6 protein).
GN Name=OSJNBa0086P08.25; Synonyms=OSJNBa0010K01.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikeno M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakemichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojohori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AF002855; BAB17214.1; -
DR EMBL; AF003210; BAB40093.1; -
DR Gramene; Q9FTT2; -
SQ SEQUENCE 106 AA; 12148 MW; A677EE54D485E8EC CRC64;

Query Match 100.0%; Score 23; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GQPR 4
Db          78 GQPR 81

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RESULT 70
Q9S159 PRELIMINARY; PRT; 106 AA.
AC Q9S159;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein At2g16590.
GN NameAt2g16590;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RN
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
RA Fraser C.M., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007195; AAD26488.1; -.
DR FRL; G84541; G84541.
KW Hypothetical protein.
SQ SEQUENCE 106 AA; 12519 MW; 00851E4AA6DB4363 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 55 GQPR 58

RESULT 71
Q92N21 PRELIMINARY; PRT; 106 AA.
AC Q92N21;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PUTATIVE TRANSMEMBRANE PROTEIN.
GN ORFNames=SMC04181;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA Capela D., Barloy-Hubier F., Couzy J., Bothe G., Ampe F., Batut J.,
RA Boissard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kies E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AC4591789; CAC46589.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
KW Complete proteome; Transmembrane.
SQ SEQUENCE 106 AA; 12105 MW; AEBOEAF31CDB67F4 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 72
Q7R3Y4 PRELIMINARY; PRT; 107 AA.
ID Q7R3Y4;
AC Q7R3Y4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 68 62183 61860.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RL "Draft sequence of the Giardia lamblia genome.";
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000012; EAA42044.1; -.
SQ SEQUENCE 107 AA; 11695 MW; CFC5D585B8B27648 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 97 GQPR 100

RESULT 73
Q820P4 PRELIMINARY; PRT; 108 AA.
ID Q820P4;
AC Q820P4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytochrome c, class IC: Cytochrome c, class I.
GN OrderedLocustNames=NE0736;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RX DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773(2003).
DR EMBL; BX323858; CAD84647.1; -.
DR HSSP; P82903; ICNO.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000345; CytC_heme_BS.
DR Pfam; PF00034; Cytochrom C; 1.
DR ProDom; PD004020; Cyt C.bact; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
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KW Complete proteome.
 SQ SEQUENCE 108 AA; 11550 MW; DE2337BCAA0FD793 CRC64;
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 Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 56 GQPR 59

RESULT 74
 Q9YDJ3 PRELIMINARY; PRT; 109 AA.
 AC Q9YDJ3;
 DT 01-NOV-1999 (T-EMBLrel. 12, Created)
 DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Hypothetical protein APE0920.
 GN OrderedLocusNames=APE0920;
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 OC Desulfurococaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 DR EMBL; AP000060; BAA79904.1; --
 DR PIR; H72687;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 109 AA; 12293 MW; E9BDC6919B254CF1 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 24 GQPR 27

RESULT 75
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 AC Q8S5J0;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Hypothetical protein OSJNBa0011A24.25.
 GN Names=OSJNBa0011A24.25;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoidae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McCombie W.R., de la Bastide M., Spiegel L., Preston R., Ferraro K.,
 RA Kuit K., Nascimento L., Zutavern I., Balija V., Bell M., Baker J.,
 RA Santos L., Miller B., Katzenberger F., Muller S., King L., Yang C.,
 RA Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC113336; AAM01182.2; --
 DR Gramene; Q8S5J0; --
 KW Hypothetical protein.
 SQ SEQUENCE 109 AA; 11946 MW; 4632E839B432CFE2 CRC64;
 Query Match 100.0%; Score 23; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 36 GQPR 39

Search completed: May 17, 2005, 10:08:23
 Job time : 98 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2005, 10:00:57 ; Search time 23 Seconds
(without alignments)
12.982 Million cell updates/sec

Title: US-10-731-921-3
Perfect score: 23
Sequence: 1 GQPR 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA: *
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4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/6CTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	23	100.0	9	4	US-09-435-739-8
3	23	100.0	9	4	US-09-988-113-8
4	23	100.0	10	3	US-09-181-336-1
5	23	100.0	10	3	US-09-252-586-21
6	23	100.0	14	3	US-09-261-855-3
7	23	100.0	14	4	US-09-873-637-3
8	23	100.0	18	1	US-08-471-780C-109
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22	23	100.0	18	3	US-08-468-739C-111
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24	23	100.0	18	4	US-09-293-769A-110
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57	23	100.0	37	4	US-10-115-123-262	Sequence 262, App
58	23	100.0	38	2	US-08-809-440-15	Sequence 15, Appli
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72	23	100.0	68	4	US-08-754-477A-139	Sequence 139, App
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118	23	100.0	110	4	US-09-270-767-56435	Sequence 56435, A	191	23	100.0	181	4	US-09-252-991A-23717	Sequence 23717, A
119	23	100.0	112	4	US-09-640-211A-1119	Sequence 1119, Ap	192	23	100.0	183	4	US-09-252-991A-26451	Sequence 26451, A
120	23	100.0	113	3	US-09-284-033-7	Sequence 7, Appl	193	23	100.0	184	4	US-09-902-540-10529	Sequence 10529, A
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135	23	100.0	134	4	US-09-252-991A-23970	Sequence 23970, A	208	23	100.0	202	4	US-09-489-039A-8112	Sequence 8112, App
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137	23	100.0	134	4	US-09-252-991A-31289	Sequence 31289, A	210	23	100.0	202	4	US-09-270-767-34039	Sequence 34039, A
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147	23	100.0	143	4	US-09-252-991A-32704	Sequence 32704, A	220	23	100.0	212	2	US-08-936-854-4	Sequence 4, Appl
148	23	100.0	147	4	US-09-270-767-46762	Sequence 46762, A	221	23	100.0	212	3	US-09-022-255-4	Sequence 4, Appl
149	23	100.0	148	4	US-09-252-991A-21248	Sequence 21248, A	222	23	100.0	212	3	US-09-022-696-4	Sequence 4, Appl
150	23	100.0	148	4	US-09-434-840-30	Sequence 30, Appl	223	23	100.0	212	3	US-09-022-253-4	Sequence 4, Appl
151	23	100.0	149	4	US-09-252-991A-32070	Sequence 32070, A	224	23	100.0	212	3	US-09-022-260-4	Sequence 4, Appl
152	23	100.0	153	4	US-09-252-991A-27025	Sequence 27025, A	225	23	100.0	212	3	US-09-022-259-4	Sequence 4, Appl
153	23	100.0	153	4	US-09-270-767-45238	Sequence 45238, A	226	23	100.0	212	3	US-09-022-257-4	Sequence 4, Appl
154	23	100.0	153	4	US-09-902-540-11548	Sequence 11548, A	227	23	100.0	212	4	US-09-252-991A-19448	Sequence 19448, A
155	23	100.0	154	4	US-09-252-991A-26832	Sequence 26832, A	228	23	100.0	212	4	US-09-549-679-4	Sequence 2, Appl
156	23	100.0	154	4	US-09-252-991A-31305	Sequence 31305, A	229	23	100.0	212	4	US-10-033-522-2	Sequence 2, Appl
157	23	100.0	155	4	US-09-975-456B-10	Sequence 10, Appl	230	23	100.0	213	4	US-09-252-991A-29496	Sequence 29496, A
158	23	100.0	156	4	US-09-252-991A-31384	Sequence 31384, A	231	23	100.0	213	4	US-09-328-352-6121	Sequence 6121, Ap
159	23	100.0	156	4	US-09-621-976-4844	Sequence 4844, Ap	232	23	100.0	214	4	US-09-248-796A-21566	Sequence 21566, A
160	23	100.0	159	4	US-09-252-991A-19997	Sequence 19997, A	233	23	100.0	216	4	US-09-248-796A-18824	Sequence 18824, A
161	23	100.0	160	4	US-09-270-767-31703	Sequence 31703, A	234	23	100.0	217	4	US-09-483-588-5	Sequence 5, Appl
162	23	100.0	161	4	US-09-270-767-35934	Sequence 35934, A	235	23	100.0	218	4	US-09-483-588-3	Sequence 3, Appl
163	23	100.0	161	4	US-09-270-767-51151	Sequence 51151, A	236	23	100.0	218	4	US-09-483-588-6	Sequence 6, Appl
164	23	100.0	162	4	US-09-640-211A-1104	Sequence 1104, Ap	237	23	100.0	218	4	US-09-483-588-7	Sequence 7, Appl
165	23	100.0	163	3	US-09-199-637A-335	Sequence 335, App	238	23	100.0	218	4	US-09-252-991A-17169	Sequence 17169, A
166	23	100.0	165	3	US-08-966-317-1	Sequence 1, Appl	239	23	100.0	219	4	US-09-252-991A-17855	Sequence 17855, A
167	23	100.0	165	3	US-09-489-770-1	Sequence 1, Appl	240	23	100.0	223	4	US-09-710-279-496	Sequence 496, App
168	23	100.0	165	4	US-09-902-540-13688	Sequence 13688, A	241	23	100.0	224	4	US-09-710-279-1366	Sequence 1366, Ap
169	23	100.0	166	4	US-09-252-991A-20239	Sequence 20239, A	242	23	100.0	224	4	US-09-252-991A-27348	Sequence 27348, A
170	23	100.0	169	4	US-09-252-991A-20992	Sequence 20992, A	243	23	100.0	225	4	US-09-911-853-23	Sequence 23, Appl
171	23	100.0	169	4	US-09-252-991A-22999	Sequence 22999, A	244	23	100.0	227	3	US-09-479-409-23	Sequence 23, Appl
172	23	100.0	169	4	US-09-252-991A-24746	Sequence 24746, A	245	23	100.0	227	3	US-09-479-453-23	Sequence 23, Appl
173	23	100.0	169	4	US-09-252-991A-25204	Sequence 25204, A	246	23	100.0	227	3		

247	23	100.0	227	4	US-09-461-325-211	Sequence 211, App	320	23	100.0	245	4	US-08-424-550B-40	Sequence 40, Appl
248	23	100.0	227	4	US-10-012-542-211	Sequence 211, App	321	23	100.0	246	4	US-09-252-991A-31095	Sequence 31095, A
249	23	100.0	227	4	US-10-115-123-211	Sequence 211, App	322	23	100.0	247	4	US-09-428-082B-6	Sequence 6, Appl
250	23	100.0	228	3	US-09-134-001C-5384	Sequence 5384, Ap	323	23	100.0	247	4	US-09-428-082B-12	Sequence 12, Appl
251	23	100.0	228	4	US-09-489-039A-10548	Sequence 10548, A	324	23	100.0	248	4	US-09-252-991A-19942	Sequence 19942, A
252	23	100.0	228	4	US-09-428-082B-2	Sequence 2, Appl	325	23	100.0	248	4	US-09-252-991A-21872	Sequence 21872, A
253	23	100.0	228	4	US-09-847-249A-2	Sequence 2, Appl	326	23	100.0	248	4	US-09-252-991A-30679	Sequence 30679, A
254	23	100.0	228	4	US-09-840-669B-2	Sequence 2, Appl	327	23	100.0	248	4	US-09-428-082B-1056	Sequence 1056, Ap
255	23	100.0	228	4	US-09-843-221A-2	Sequence 2, Appl	328	23	100.0	248	4	US-09-428-082B-1058	Sequence 1058, Ap
256	23	100.0	228	4	US-09-968-362A-27	Sequence 27, Appl	329	23	100.0	248	4	US-09-428-082B-1060	Sequence 1060, Ap
257	23	100.0	228	4	US-09-709-704B-2	Sequence 2, Appl	330	23	100.0	248	4	US-09-428-082B-1062	Sequence 1062, Ap
258	23	100.0	228	4	US-09-422-838C-5	Sequence 5, Appl	331	23	100.0	250	4	US-09-428-082B-1070	Sequence 1070, Ap
259	23	100.0	229	4	US-09-122-144-2	Sequence 2, Appl	332	23	100.0	250	4	US-09-248-796A-27542	Sequence 27542, A
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261	23	100.0	229	4	US-09-252-991A-27802	Sequence 27802, A	334	23	100.0	252	4	US-09-428-082B-1066	Sequence 1066, Ap
262	23	100.0	229	4	US-09-252-991A-27907	Sequence 27907, A	335	23	100.0	252	4	US-09-976-594-112	Sequence 112, App
263	23	100.0	229	4	US-09-968-362A-28	Sequence 28, Appl	336	23	100.0	253	4	US-09-252-991A-26659	Sequence 26659, A
264	23	100.0	230	4	US-09-252-991A-16763	Sequence 16763, A	337	23	100.0	253	4	US-09-428-082B-16	Sequence 16, Appl
265	23	100.0	230	4	US-09-252-991A-28838	Sequence 28838, A	338	23	100.0	253	4	US-09-428-082B-18	Sequence 18, Appl
266	23	100.0	231	4	US-09-252-991A-22663	Sequence 22663, A	339	23	100.0	254	4	US-08-284-391B-33	Sequence 33, Appl
267	23	100.0	231	4	US-09-252-991A-22962	Sequence 22962, A	340	23	100.0	254	3	US-09-218-950-33	Sequence 33, Appl
268	23	100.0	231	4	US-09-248-796A-27586	Sequence 27586, A	341	23	100.0	254	4	US-09-252-991A-25445	Sequence 25445, A
269	23	100.0	232	1	US-07-797-556-4	Sequence 4, Appl	342	23	100.0	254	4	US-09-252-991A-32919	Sequence 32919, A
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271	23	100.0	232	1	US-08-570-923-4	Sequence 4, Appl	344	23	100.0	256	4	US-09-252-991A-29557	Sequence 29557, A
272	23	100.0	232	1	US-08-580-014-4	Sequence 4, Appl	345	23	100.0	256	4	US-09-902-540-11957	Sequence 11957, A
273	23	100.0	232	1	US-08-308-881-4	Sequence 4, Appl	346	23	100.0	256	4	US-09-252-991A-25689	Sequence 25689, A
274	23	100.0	232	2	US-09-058-263-4	Sequence 4, Appl	347	23	100.0	259	4	US-09-808-701A-18	Sequence 18, Appl
275	23	100.0	232	2	US-09-059-099-4	Sequence 4, Appl	348	23	100.0	260	4	US-09-071-252-12	Sequence 12, Appl
276	23	100.0	232	2	US-08-595-043A-50	Sequence 50, Appl	349	23	100.0	261	4	US-09-252-991A-16803	Sequence 16803, A
277	23	100.0	232	3	US-09-058-264-4	Sequence 4, Appl	350	23	100.0	261	4	US-09-252-991A-23563	Sequence 23563, A
278	23	100.0	232	3	US-08-996-139-8	Sequence 8, Appl	351	23	100.0	261	4	US-09-071-252-10	Sequence 10, Appl
279	23	100.0	232	3	US-09-079-785-4	Sequence 4, Appl	352	23	100.0	262	4	US-09-902-540-11432	Sequence 11432, A
280	23	100.0	232	3	US-08-995-659-8	Sequence 8, Appl	353	23	100.0	263	4	US-09-818-780-32	Sequence 32, Appl
281	23	100.0	232	3	US-09-215-649A-8	Sequence 8, Appl	354	23	100.0	263	4	US-09-818-780-88	Sequence 88, Appl
282	23	100.0	232	4	US-09-577-780-8	Sequence 8, Appl	355	23	100.0	263	4	US-09-270-767-32374	Sequence 32374, A
283	23	100.0	232	4	US-09-577-800-8	Sequence 8, Appl	356	23	100.0	263	4	US-09-270-767-47591	Sequence 47591, A
284	23	100.0	232	4	US-09-455-962-4	Sequence 4, Appl	357	23	100.0	264	4	US-09-252-991A-30092	Sequence 30092, A
285	23	100.0	232	4	US-09-466-496-8	Sequence 4, Appl	358	23	100.0	265	4	US-09-252-991A-29150	Sequence 29150, A
286	23	100.0	232	4	US-09-871-856-8	Sequence 8, Appl	359	23	100.0	268	4	US-09-428-082B-8	Sequence 8, Appl
287	23	100.0	232	4	US-09-252-991A-17146	Sequence 17146, A	360	23	100.0	269	2	US-08-727-311-3	Sequence 3, Appl
288	23	100.0	232	4	US-09-871-291-8	Sequence 8, Appl	361	23	100.0	269	3	US-09-111-556A-4	Sequence 4, Appl
289	23	100.0	232	4	US-09-877-650-8	Sequence 4, Appl	362	23	100.0	269	4	US-08-360-758-4	Sequence 4, Appl
290	23	100.0	232	4	US-09-628-126-4	Sequence 4, Appl	363	23	100.0	269	4	US-09-252-991A-20973	Sequence 20973, A
291	23	100.0	232	4	US-09-865-363-8	Sequence 8, Appl	364	23	100.0	269	4	US-09-428-082B-10	Sequence 10, Appl
292	23	100.0	232	4	US-09-968-362A-26	Sequence 26, Appl	365	23	100.0	269	4	US-09-422-838C-46	Sequence 46, Appl
293	23	100.0	232	4	US-09-688-459-8	Sequence 8, Appl	366	23	100.0	270	4	US-09-252-991A-18185	Sequence 18185, A
294	23	100.0	232	5	PCT-US95-06530-4	Sequence 4, Appl	367	23	100.0	270	4	US-09-540-236-3122	Sequence 3122, Ap
295	23	100.0	232	5	PCT-US95-15781-8	Sequence 8, Appl	368	23	100.0	271	4	US-09-252-991A-29010	Sequence 29010, A
296	23	100.0	234	4	US-08-756-416-33	Sequence 33, Appl	369	23	100.0	272	4	US-09-252-991A-31806	Sequence 31806, A
297	23	100.0	235	1	US-08-591-989-2	Sequence 2, Appl	370	23	100.0	273	4	US-09-252-991A-16693	Sequence 16693, A
298	23	100.0	235	3	US-09-131-247-6	Sequence 6, Appl	371	23	100.0	273	4	US-09-252-991A-17447	Sequence 17447, A
299	23	100.0	235	4	US-09-784-623-6	Sequence 6, Appl	372	23	100.0	273	4	US-09-252-991A-22485	Sequence 22485, A
300	23	100.0	235	4	US-09-302-540-11606	Sequence 11606, A	373	23	100.0	273	4	US-09-252-991A-32405	Sequence 32405, A
301	23	100.0	238	4	US-09-134-000C-6559	Sequence 6559, Ap	374	23	100.0	275	4	US-09-252-991A-17995	Sequence 17995, A
302	23	100.0	239	4	US-09-252-991A-26949	Sequence 26949, A	375	23	100.0	276	4	US-09-252-991A-23623	Sequence 23623, A
303	23	100.0	240	4	US-09-252-991A-17237	Sequence 17237, A	376	23	100.0	277	4	US-09-428-082B-20	Sequence 20, Appl
304	23	100.0	240	4	US-09-252-991A-17701	Sequence 17701, A	377	23	100.0	277	4	US-09-428-082B-22	Sequence 22, Appl
305	23	100.0	240	4	US-09-252-991A-19090	Sequence 19090, A	378	23	100.0	279	4	US-09-252-991A-32443	Sequence 32443, A
306	23	100.0	240	4	US-09-270-767-57173	Sequence 57173, A	379	23	100.0	281	4	US-09-252-991A-17748	Sequence 17748, A
307	23	100.0	241	4	US-09-640-211A-819	Sequence 819, App	380	23	100.0	281	4	US-09-854-864-10	Sequence 10, Appl
308	23	100.0	242	4	US-09-252-991A-32268	Sequence 32268, A	381	23	100.0	282	4	US-09-252-991A-28598	Sequence 28598, A
309	23	100.0	243	4	US-09-428-082B-1068	Sequence 1068, Ap	382	23	100.0	282	4	US-09-949-016-8392	Sequence 8392, Ap
310	23	100.0	243	4	US-09-252-991A-13234	Sequence 13234, A	383	23	100.0	283	4	US-09-387-375-7	Sequence 7, Appl
311	23	100.0	243	1	US-07-943-843-8	Sequence 8, Appl	384	23	100.0	284	4	US-10-041-400A-7	Sequence 7, Appl
312	23	100.0	245	1	US-08-236-918A-15	Sequence 15, Appl	385	23	100.0	284	4	US-10-042-991A-7	Sequence 7, Appl
313	23	100.0	245	1	US-08-347-003-8	Sequence 8, Appl	386	23	100.0	286	4	US-09-252-991A-24111	Sequence 24111, A
314	23	100.0	245	3	US-09-150-864A-15	Sequence 15, Appl	387	23	100.0	286	4	US-09-252-991A-30343	Sequence 30343, A
315	23	100.0	245	4	US-08-469-260A-40	Sequence 40, Appl	388	23	100.0	287	4	US-09-252-991A-19944	Sequence 19944, A
316	23	100.0	245	4	US-08-488-446-40	Sequence 40, Appl	389	23	100.0	287	4	US-09-252-991A-17482	Sequence 17482, A
317	23	100.0	245	4	US-08-467-344A-40	Sequence 40, Appl	390	23	100.0	289	4	US-09-252-991A-23728	Sequence 23728, A
318	23	100.0	245	4	US-09-489-039A-14192	Sequence 14192, A	391	23	100.0	290	4	US-08-484-841A-8	Sequence 8, Appl
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393	23	100.0	291	4	US-09-007-288E-119	Sequence 119, App	466	23	100.0	331	4	US-09-252-991A-23301	Sequence 23301, A
394	23	100.0	291	4	US-09-252-991A-19371	Sequence 19371, A	467	23	100.0	331	4	US-09-328-352-991A-5339	Sequence 5339, Ap
395	23	100.0	293	4	US-09-252-991A-32060	Sequence 32060, A	468	23	100.0	331	4	US-09-467-638-5	Sequence 5, Appli
396	23	100.0	294	4	US-09-252-991A-18089	Sequence 18089, A	469	23	100.0	331	4	US-09-467-638-7	Sequence 7, Appli
397	23	100.0	295	4	US-09-270-767-44257	Sequence 44257, A	470	23	100.0	331	4	US-09-640-211A-1073	Sequence 1073, Ap
398	23	100.0	297	4	US-09-252-991A-24412	Sequence 24412, A	471	23	100.0	332	4	US-09-252-991A-28896	Sequence 28896, A
399	23	100.0	297	4	US-09-252-991A-27909	Sequence 27909, A	472	23	100.0	332	4	US-09-252-991A-31956	Sequence 31956, A
400	23	100.0	297	4	US-09-252-991A-29217	Sequence 29217, A	473	23	100.0	336	2	US-08-784-651-2	Sequence 2, Appli
401	23	100.0	298	4	US-09-252-991A-19908	Sequence 19908, A	474	23	100.0	336	2	US-08-784-651-4	Sequence 4, Appli
402	23	100.0	298	4	US-09-252-991A-31102	Sequence 31102, A	475	23	100.0	336	4	US-09-007-288E-122	Sequence 122, App
403	23	100.0	299	4	US-09-520-781-28	Sequence 28, Appl	476	23	100.0	336	4	US-09-252-991A-25385	Sequence 25385, A
404	23	100.0	300	4	US-09-252-991A-28367	Sequence 28367, A	477	23	100.0	337	2	US-08-784-651-8	Sequence 8, Appli
405	23	100.0	300	4	US-09-883-777-9	Sequence 9, Appli	478	23	100.0	337	4	US-09-252-991A-17436	Sequence 17436, A
406	23	100.0	301	4	US-09-252-991A-18428	Sequence 18428, A	479	23	100.0	338	2	US-08-784-651-6	Sequence 6, Appli
407	23	100.0	302	4	US-09-252-991A-15900	Sequence 15900, A	480	23	100.0	338	2	US-08-784-651-10	Sequence 10, Appl
408	23	100.0	302	4	US-09-252-991A-22563	Sequence 22563, A	481	23	100.0	338	4	US-09-540-236-3716	Sequence 3716, Ap
409	23	100.0	302	4	US-09-252-991A-23166	Sequence 23166, A	482	23	100.0	339	4	US-09-252-991A-25435	Sequence 25435, A
410	23	100.0	305	4	US-09-252-991A-17408	Sequence 17408, A	483	23	100.0	339	4	US-09-902-540-16772	Sequence 16772, A
411	23	100.0	305	4	US-09-252-991A-18762	Sequence 18762, A	484	23	100.0	340	4	US-09-489-039A-12325	Sequence 12325, A
412	23	100.0	305	4	US-09-252-991A-20357	Sequence 20357, A	485	23	100.0	341	4	US-09-252-991A-20182	Sequence 20182, A
413	23	100.0	306	4	US-09-252-991A-22019	Sequence 22019, A	486	23	100.0	341	4	US-09-252-991A-27955	Sequence 27955, A
414	23	100.0	306	4	US-09-489-039A-8745	Sequence 8745, Ap	487	23	100.0	342	4	US-09-252-991A-19222	Sequence 19222, A
415	23	100.0	307	4	US-09-252-991A-21588	Sequence 21588, A	488	23	100.0	342	4	US-09-107-532A-6412	Sequence 6412, Ap
416	23	100.0	307	4	US-09-252-991A-28821	Sequence 28821, A	489	23	100.0	344	4	US-09-252-991A-24996	Sequence 24996, A
417	23	100.0	309	4	US-09-252-991A-23189	Sequence 23189, A	490	23	100.0	345	4	US-08-311-731A-292	Sequence 292, App
418	23	100.0	309	4	US-09-252-991A-27042	Sequence 27042, A	491	23	100.0	346	1	US-07-621-193A-3	Sequence 3, Appli
419	23	100.0	309	4	US-09-883-777-7	Sequence 7, Appli	492	23	100.0	346	1	US-08-018-489C-3	Sequence 3, Appli
420	23	100.0	309	4	US-09-742-454A-7	Sequence 7, Appli	493	23	100.0	346	4	US-09-252-991A-22101	Sequence 22101, A
421	23	100.0	310	4	US-09-252-991A-32782	Sequence 32782, A	494	23	100.0	346	4	US-09-252-991A-29956	Sequence 29956, A
422	23	100.0	311	4	US-09-252-991A-29142	Sequence 29142, A	495	23	100.0	346	4	US-09-252-991A-31323	Sequence 31323, A
423	23	100.0	311	4	US-09-489-039A-13862	Sequence 13862, A	496	23	100.0	347	1	US-07-940-861-43	Sequence 43, Appl
424	23	100.0	313	3	US-08-713-556P-36	Sequence 36, Appl	497	23	100.0	347	1	US-08-459-513-43	Sequence 43, Appl
425	23	100.0	314	2	US-08-525-742-6	Sequence 6, Appli	498	23	100.0	347	2	US-08-459-657-43	Sequence 43, Appl
426	23	100.0	314	4	US-09-252-991A-18489	Sequence 18489, A	499	23	100.0	347	2	US-08-460-132-43	Sequence 43, Appl
427	23	100.0	314	4	US-09-252-991A-18752	Sequence 18752, A	500	23	100.0	347	3	US-08-466-465-8	Sequence 8, Appli
428	23	100.0	314	4	US-09-252-991A-20243	Sequence 20243, A	501	23	100.0	347	5	PCT-US92-02050-43	Sequence 43, Appl
429	23	100.0	314	4	US-09-252-991A-31938	Sequence 31938, A	502	23	100.0	347	5	US-09-252-991A-25327	Sequence 25327, A
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431	23	100.0	316	4	US-09-761-413-4	Sequence 4, Appli	504	23	100.0	350	4	US-09-252-991A-17132	Sequence 17132, A
432	23	100.0	318	4	US-09-252-991A-22047	Sequence 22047, A	505	23	100.0	350	4	US-09-902-540-15821	Sequence 15821, A
433	23	100.0	318	4	US-09-252-991A-23374	Sequence 23374, A	506	23	100.0	350	5	PCT-US95-08745-14	Sequence 14, Appl
434	23	100.0	318	4	US-09-252-991A-23557	Sequence 23557, A	507	23	100.0	352	4	US-09-252-991A-24722	Sequence 24722, A
435	23	100.0	318	4	US-09-252-991A-32374	Sequence 32374, A	508	23	100.0	352	3	US-09-116-115-17	Sequence 17, Appl
436	23	100.0	319	4	US-09-252-991A-21656	Sequence 21656, A	509	23	100.0	357	3	US-09-541-762-17	Sequence 17, Appl
437	23	100.0	319	4	US-09-252-991A-23566	Sequence 23566, A	510	23	100.0	357	4	US-09-270-767-41923	Sequence 41923, A
438	23	100.0	320	4	US-09-252-991A-23403	Sequence 23403, A	511	23	100.0	358	4	US-09-328-352-4311	Sequence 4311, Ap
439	23	100.0	320	4	US-09-949-016-11458	Sequence 11458, A	512	23	100.0	359	4	US-09-180-100-11	Sequence 11, Appl
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443	23	100.0	322	4	US-09-840-211A-784	Sequence 784, App	516	23	100.0	362	4	US-09-252-991A-26561	Sequence 26561, A
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446	23	100.0	324	4	US-09-252-991A-32530	Sequence 32530, A	519	23	100.0	363	4	US-09-252-991A-23199	Sequence 23199, A
447	23	100.0	325	4	US-08-656-586-9	Sequence 9, Appli	520	23	100.0	363	4	US-09-489-039A-8168	Sequence 8168, Ap
448	23	100.0	326	2	US-08-986-217-3	Sequence 3, Appli	521	23	100.0	364	4	US-09-543-681A-7525	Sequence 7525, Ap
449	23	100.0	326	3	US-08-808-720-3	Sequence 3, Appli	522	23	100.0	364	4	US-09-472-087-100	Sequence 100, App
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453	23	100.0	327	3	US-08-808-720-1	Sequence 1, Appli	526	23	100.0	371	2	US-08-948-176-26	Sequence 26, Appl
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455	23	100.0	328	4	US-09-467-638-1	Sequence 1, Appli	528	23	100.0	371	4	US-10-157-408-7	Sequence 7, Appli
456	23	100.0	329	4	US-09-313-942-12	Sequence 12, Appl	529	23	100.0	372	4	US-09-252-991A-20371	Sequence 20371, A
457	23	100.0	329	4	US-09-301-593-22	Sequence 22, Appl	530	23	100.0	372	4	US-09-252-991A-27599	Sequence 27599, A
458	23	100.0	330	4	US-09-252-991A-23331	Sequence 23331, A	531	23	100.0	374	4	US-09-227-595-26	Sequence 26, Appl
459	23	100.0	330	4	US-09-252-991A-28827	Sequence 28827, A	532	23	100.0	374	4	US-09-227-595-28	Sequence 28, Appl
460	23	100.0	330	4	US-09-248-796A-19977	Sequence 19977, A	533	23	100.0	374	4	US-08-595-590B-26	Sequence 26, Appl
461	23	100.0	331	3	US-08-808-720-5	Sequence 5, Appli	534	23	100.0	374	4	US-08-595-590B-28	Sequence 28, Appl
462	23	100.0	331	3	US-08-808-720-7	Sequence 7, Appli	535	23	100.0	375	4	US-09-328-352-8119	Sequence 8119, Ap
463	23	100.0	331	3	US-09-178-869-2	Sequence 2, Appli	536	23	100.0	375	4	US-09-976-594-795	Sequence 795, App
464	23	100.0	331	4	US-09-761-413-2	Sequence 2, Appli	537	23	100.0	375	4	US-09-538-092-1244	Sequence 1244, Ap
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543	23	100.0	377	4	US-09-227-595-24	Sequence 24, Appl	616	23	100.0	423	4	US-09-832-659A-44	Sequence 44, Appl
544	23	100.0	377	4	US-08-595-390B-24	Sequence 24, Appl	617	23	100.0	424	3	US-09-333-593A-8	Sequence 8, Appl
545	23	100.0	377	4	US-09-949-016-10067	Sequence 10067, A	618	23	100.0	424	5	PCT-US95-03866-12	Sequence 12, Appl
546	23	100.0	377	4	US-09-949-016-10068	Sequence 10068, A	619	23	100.0	424	5	PCT-US95-03866-14	Sequence 14, Appl
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548	23	100.0	380	3	US-09-181-336-19	Sequence 19, Appl	621	23	100.0	425	4	US-09-902-540-13785	Sequence 13785, A
549	23	100.0	381	4	US-09-252-991A-28320	Sequence 28320, A	622	23	100.0	429	2	US-09-074-512-1	Sequence 1, Appl
550	23	100.0	382	1	US-08-470-299-7	Sequence 7, Appl	623	23	100.0	429	4	US-09-372-425A-6	Sequence 6, Appl
551	23	100.0	382	1	US-08-470-299-10	Sequence 10, Appl	624	23	100.0	429	4	US-09-489-039A-10891	Sequence 10891, A
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557	23	100.0	388	4	US-09-252-991A-21876	Sequence 21876, A	630	23	100.0	432	3	US-08-477-460B-2	Sequence 2, Appl
558	23	100.0	388	4	US-09-252-991A-24693	Sequence 24693, A	631	23	100.0	432	3	US-08-379-516-2	Sequence 2, Appl
559	23	100.0	388	4	US-09-784-623-16	Sequence 16, Appl	632	23	100.0	432	3	US-09-329-916-2	Sequence 2, Appl
560	23	100.0	389	3	US-09-131-247-14	Sequence 14, Appl	633	23	100.0	432	3	US-08-485-372A-2	Sequence 2, Appl
561	23	100.0	389	4	US-09-252-991A-30972	Sequence 30972, A	634	23	100.0	432	3	US-09-409-006A-2	Sequence 2, Appl
562	23	100.0	389	4	US-09-784-623-14	Sequence 14, Appl	635	23	100.0	432	4	US-08-484-681-2	Sequence 2, Appl
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564	23	100.0	392	4	US-09-252-991A-31291	Sequence 31291, A	637	23	100.0	432	4	US-09-252-991A-32301	Sequence 32301, A
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566	23	100.0	393	3	US-09-058-376-4	Sequence 4, Appl	639	23	100.0	432	5	PCT-US93-07422-2	Sequence 2, Appl
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571	23	100.0	396	3	US-09-176-228-3	Sequence 3, Appl	644	23	100.0	434	4	US-09-252-991A-24980	Sequence 24980, A
572	23	100.0	396	4	US-09-252-991A-24697	Sequence 24697, A	645	23	100.0	434	4	US-08-472-888A-4	Sequence 4, Appl
573	23	100.0	397	4	US-08-775-066-2	Sequence 2, Appl	646	23	100.0	436	4	US-09-734-673-2	Sequence 2, Appl
574	23	100.0	397	4	US-09-854-864-18	Sequence 18, Appl	647	23	100.0	436	4	US-09-523-849-2	Sequence 2, Appl
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576	23	100.0	397	4	US-09-949-016-11172	Sequence 11172, A	649	23	100.0	437	4	US-09-252-991A-24390	Sequence 24390, A
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578	23	100.0	399	4	US-09-252-991A-16821	Sequence 16821, A	651	23	100.0	437	5	US-08-097-827-11	Sequence 11, Appl
579	23	100.0	399	4	US-09-252-991A-21997	Sequence 21997, A	652	23	100.0	438	1	US-08-494-574-11	Sequence 11, Appl
580	23	100.0	399	4	US-09-252-991A-28212	Sequence 28212, A	653	23	100.0	438	1	US-09-252-991A-28398	Sequence 28398, A
581	23	100.0	399	4	US-09-832-659A-2	Sequence 2, Appl	654	23	100.0	438	4	US-09-543-681A-4367	Sequence 4367, Ap
582	23	100.0	400	2	US-08-733-825-2	Sequence 2, Appl	655	23	100.0	438	4	US-09-252-991A-31919	Sequence 31919, A
583	23	100.0	400	4	US-09-252-991A-31900	Sequence 31900, A	656	23	100.0	439	4	US-09-252-991A-28965	Sequence 28965, A
584	23	100.0	400	4	US-09-949-016-6685	Sequence 6685, Ap	657	23	100.0	441	4	US-08-480-036-2	Sequence 2, Appl
585	23	100.0	401	4	US-09-270-767-37634	Sequence 37634, A	658	23	100.0	442	1	US-08-461-968A-5	Sequence 5, Appl
586	23	100.0	401	4	US-09-270-767-52851	Sequence 52851, A	659	23	100.0	442	1	US-08-462-571-2	Sequence 2, Appl
587	23	100.0	401	4	US-09-248-796A-19514	Sequence 19514, A	660	23	100.0	442	2	US-08-462-571-5	Sequence 5, Appl
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589	23	100.0	402	4	US-09-489-039A-9618	Sequence 9618, Ap	662	23	100.0	442	4	US-08-472-888A-2	Sequence 2, Appl
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591	23	100.0	403	4	US-09-489-039A-12412	Sequence 12412, A	664	23	100.0	442	5	PCT-US96-10043-9	Sequence 9, Appl
592	23	100.0	404	4	US-09-252-991A-18789	Sequence 18789, A	665	23	100.0	442	5	PCT-US96-10043-12	Sequence 12, Appl
593	23	100.0	405	4	US-09-489-039A-7341	Sequence 7341, Ap	666	23	100.0	442	5	US-09-949-016-11352	Sequence 11352, A
594	23	100.0	406	4	US-09-949-016-10207	Sequence 10207, A	667	23	100.0	443	4	US-09-252-991A-28809	Sequence 28809, A
595	23	100.0	407	4	US-09-252-991A-32423	Sequence 32423, A	668	23	100.0	443	5	US-09-328-352-7043	Sequence 7043, Ap
596	23	100.0	408	4	US-09-252-991A-27849	Sequence 27849, A	669	23	100.0	444	4	US-08-341-560B-17	Sequence 17, Appl
597	23	100.0	408	4	US-09-489-039A-8307	Sequence 8307, Ap	670	23	100.0	444	4	US-09-252-991A-28706	Sequence 28706, A
598	23	100.0	409	4	US-09-252-991A-26859	Sequence 26859, A	671	23	100.0	444	3	US-08-397-411-7	Sequence 7, Appl
599	23	100.0	409	4	US-09-328-352-4570	Sequence 4570, Ap	672	23	100.0	445	4	US-09-157-452B-12	Sequence 12, Appl
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607	23	100.0	415	4	US-09-248-796A-17467	Sequence 17467, A	680	23	100.0	449	1	US-08-458-516-13	Sequence 13, Appl
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610	23	100.0	418	4	US-09-832-659A-42	Sequence 42, Appl	683	23	100.0	449			
611	23	100.0	418	4	US-09-949-016-8510	Sequence 8510, Ap	684	23	100.0	449			

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686	23	100.0	449	4	US-09-680-148-2	Sequence 2, Appli	759	453	4	US-09-802-070-8	Sequence 8, Appli
687	23	100.0	449	4	US-09-304-465A-2	Sequence 2, Appli	760	453	4	US-10-212-507-6	Sequence 6, Appli
688	23	100.0	449	4	US-09-500-253B-23	Sequence 23, Appli	761	454	2	US-07-934-373C-22	Sequence 22, Appli
689	23	100.0	449	4	US-09-368-362A-20	Sequence 20, Appli	762	454	3	US-08-437-642B-22	Sequence 22, Appli
690	23	100.0	450	2	US-08-768-800-12	Sequence 12, Appli	763	454	3	US-08-146-206C-22	Sequence 22, Appli
691	23	100.0	450	4	US-09-532-856-5	Sequence 5, Appli	764	454	4	US-09-252-991A-28780	Sequence 28780, A
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693	23	100.0	450	4	US-09-324-100C-5	Sequence 5, Appli	766	454	4	US-09-705-392A-22	Sequence 22, Appli
694	23	100.0	450	4	US-10-212-507-5	Sequence 5, Appli	767	454	4	US-09-705-398-22	Sequence 22, Appli
695	23	100.0	450	4	US-09-996-288-208	Sequence 208, App	768	454	5	PCF-US93-0783B-22	Sequence 22, Appli
696	23	100.0	450	4	US-09-996-288-210	Sequence 210, App	769	455	4	US-09-773-877B-24	Sequence 24, Appli
697	23	100.0	450	4	US-09-996-288-212	Sequence 212, App	770	455	4	US-09-252-991A-17335	Sequence 17335, A
698	23	100.0	450	4	US-09-996-288-214	Sequence 214, App	771	458	4	US-09-773-877B-22	Sequence 22, Appli
699	23	100.0	450	4	US-09-996-288-216	Sequence 216, App	772	458	4	US-09-773-877B-26	Sequence 26, Appli
700	23	100.0	450	4	US-09-996-288-218	Sequence 218, App	773	459	1	US-08-157-101A-7	Sequence 7, Appli
701	23	100.0	450	4	US-09-996-288-220	Sequence 220, App	774	461	4	US-09-252-991A-24667	Sequence 24667, A
702	23	100.0	450	4	US-09-996-288-222	Sequence 222, App	775	462	4	US-09-289-942A-7	Sequence 7, Appli
703	23	100.0	450	4	US-09-996-288-224	Sequence 224, App	776	462	4	US-09-252-991A-31817	Sequence 31817, A
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705	23	100.0	450	4	US-09-996-288-228	Sequence 228, App	778	462	4	US-09-773-877B-18	Sequence 18, Appli
706	23	100.0	450	4	US-09-996-288-232	Sequence 232, App	779	463	4	US-09-472-087-1	Sequence 1, Appli
707	23	100.0	450	4	US-09-996-288-234	Sequence 234, App	780	463	4	US-09-472-087-4	Sequence 4, Appli
708	23	100.0	450	4	US-09-996-288-236	Sequence 236, App	781	463	4	US-09-472-087-63	Sequence 63, Appli
709	23	100.0	450	4	US-09-996-288-238	Sequence 238, App	782	463	4	US-09-472-087-64	Sequence 64, Appli
710	23	100.0	450	4	US-09-996-288-240	Sequence 240, App	783	463	4	US-09-472-087-68	Sequence 68, Appli
711	23	100.0	450	4	US-09-996-288-242	Sequence 242, App	784	464	4	US-09-252-991A-27367	Sequence 27367, A
712	23	100.0	450	4	US-09-996-288-244	Sequence 244, App	785	464	4	US-09-472-087-2	Sequence 2, Appli
713	23	100.0	450	4	US-09-996-288-246	Sequence 246, App	786	464	4	US-09-472-087-66	Sequence 66, Appli
714	23	100.0	450	4	US-09-996-288-248	Sequence 248, App	787	465	4	US-09-252-991A-20576	Sequence 20576, A
715	23	100.0	450	4	US-09-996-288-250	Sequence 250, App	788	466	4	US-09-698-705-11	Sequence 11, Appli
716	23	100.0	450	4	US-09-996-288-252	Sequence 252, App	789	467	1	US-09-704-744-81	Sequence 81, Appli
717	23	100.0	450	4	US-09-996-288-254	Sequence 254, App	790	467	3	US-09-049-672A-8	Sequence 8, Appli
718	23	100.0	451	2	US-09-996-288-256	Sequence 256, App	791	467	3	US-08-523-894-8	Sequence 8, Appli
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999 23 100.0 590 4 US-10-158-895-15 Sequence 15, Appl
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ALIGNMENTS

RESULT 1
US-08-922-170B-8
; Sequence 8, Application US/08922170B
; Patent No. 5988822
; GENERAL INFORMATION:
; APPLICANT: Iris Pecker, Israel Vlodavsky and Elena
; APPLICANT: Feinstein
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE
; TITLE OF INVENTION: HAVING HEPARANASE ACTIVITY AND EXPRESSION OF
; TITLE OF INVENTION: SAME IN TRANSFUSED CELLS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein
; STREET: 2940 Birchtree lane
; CITY: Silver Spring
; STATE: Maryland
; COUNTRY: United States of America
; ZIP: 20906
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.11
; SOFTWARE: word for Windows version 2.0 converted to
; SOFTWARE: an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/922,170B
; FILING DATE: 2 SEP 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
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; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-922-170B-8
Query Match 100.0%; Score 23; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 6 GQPR 9
RESULT 2
US-09-435-739-8
; Sequence 8, Application US/09435739
; Patent No. 6664105
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 00/20454
; CURRENT APPLICATION NUMBER: US/09/435,739
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-435-739-8
Query Match 100.0%; Score 23; DB 4; Length 9;
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RESULT 3
US-09-988-113-8
; Sequence 8, Application US/09988113
; Patent No. 6790658
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 01/22781
; CURRENT APPLICATION NUMBER: US/09/988,113
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 09/776,874
; PRIOR FILING DATE: 2001-02-06
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; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

; OTHER INFORMATION: Peptide derived from tryptic digestion of human heparanase
US-09-988-113-8

Query Match 100.0%; Score 23; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 41e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 6 GQPR 9

RESULT 4

US-09-181-336-1
; Sequence 1, Application US/09181336A
; Patent No. 6242238
; GENERAL INFORMATION:
; APPLICANT: FREEMAN, Craig Geoffrey
; APPLICANT: PARISH, Richard
; APPLICANT: HAMMORF, Brenton James
; APPLICANT: HULETT, Mark Darren
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE ENCODING MAMMALIAN
; TITLE OF INVENTION: ENDOGLUCURONIDASE AND USES THEREFOR
; FILE REFERENCE: 032505-004
; CURRENT APPLICATION NUMBER: US/09/181,336A
; CURRENT FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: AU PP0062
; EARLIER FILING DATE: 1997-10-28
; EARLIER APPLICATION NUMBER: AU PP0812
; EARLIER FILING DATE: 1997-12-09
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE
US-09-181-336-1

Query Match 100.0%; Score 23; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 7 GQPR 10

RESULT 5

US-09-252-586-21
; Sequence 21, Application US/09252586
; Patent No. 6387643
; GENERAL INFORMATION:
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Fairbanks, Michael B.
; APPLICANT: Mildner, Ana M.
; TITLE OF INVENTION: Human Platelet Heparanase Polypeptides,
; TITLE OF INVENTION: Polynucleotide Molecules That Encode Them, and Methods For
; TITLE OF INVENTION: the Identification of Compounds That Alter Heparanase
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn
; STREET: 301 Henrietta
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/252,586
; FILING DATE:
; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: Kerber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6131.N CN1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616-833-0974
; TELEFAX: 616-833-8897

; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-09-252-586-21

Query Match 100.0%; Score 23; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 7 GQPR 10

RESULT 6

US-09-261-855-3
; Sequence 3, Application US/09261855A
; Patent No. 6255055
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/261,855A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-261-855-3

Query Match 100.0%; Score 23; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 9 GQPR 12

RESULT 7

US-09-873-637-3
; Sequence 3, Application US/09873637
; Patent No. 6794151
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/873,637
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 14

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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-873-637-3

Query Match      100.0%; Score 23; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      |||||
        9 GQPR 12

RESULT 8
US-08-471-780C-109
; Sequence 109, Application US/08471780C
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,780C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-471-780C-110

Query Match      100.0%; Score 23; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      |||||
        1 GQPR 4

RESULT 10
US-08-471-780C-111
; Sequence 111, Application US/08471780C
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```


OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Hamers, Raymond
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-471-780C-111

Query Match 100.0%; Score 23; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 11
US-08-467-282B-109
Sequence 109, Application US/08467282B
Patent No. 5800988
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,282B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-467-282B-110

REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-467-282B-109

Query Match 100.0%; Score 23; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 12
US-08-467-282B-110
Sequence 110, Application US/08467282B
Patent No. 5800988
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,282B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-467-282B-110

Query Match 100.0%; Score 23; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 13
US-08-467-282B-111
; Sequence 111, Application US/08467282B
; Patent No. 5800988
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US/08/467,282B
; FILING DATE: 21-AUG-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4000
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-467-282B-111

Query Match 100.0%; Score 23; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 14
US-08-471-282A-109
; Sequence 109, Application US/08471282A
; Patent No. 5840853
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US/08/471,282A
; FILING DATE: 21-AUG-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4000
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-467-282B-111

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US/08/471,282A
; FILING DATE: 21-AUG-1992
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4000
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-471-282A-109

Query Match 100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 15
US-08-471-282A-110
; Sequence 110, Application US/08471282A
; Patent No. 5840853
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,282A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-471-282A-110

Query Match 100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 16
US-08-471-282A-111
Sequence 111, Application US/08471282A
Patent No. 5840853
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,282A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-471-282A-111
Query Match 100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 17
US-08-466-710C-109
Sequence 109, Application US/08466710C
Patent No. 5874541
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,710C
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-710C-109

Query Match 100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 18

US-08-466-710C-110
; Sequence 110, Application US/08466710C
; Patent No. 5874541
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,710C
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-466-710C-110
Query Match 100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 1 GQPR 4
RESULT 19
US-08-466-710C-111
; Sequence 111, Application US/08466710C
; Patent No. 5874541
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,710C
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-710C-111
Query Match 100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 1 GQPR 4
RESULT 20
US-08-466-739C-109
; Sequence 109, Application US/08468739C
; Patent No. 6015695
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,739C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993

```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E.R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 109:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-468-739C-109

Query Match 100.0%; Score 23; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
1 GQPR 4

RESULT 21
US-08-468-739C-110
; Sequence 110, Application US/08468739C
; Patent No. 6015695
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-468-739C-111

Query Match 100.0%; Score 23; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
1 GQPR 4

RESULT 23
US-09-293-769A-109
; Sequence 109, Application US/09293769A
; Patent No. 6765087
; GENERAL INFORMATION:
; APPLICANT: CASTERMAN, CECILE
; APPLICANT: HAMERS, RAYMOND
; TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
```

FILE REFERENCE: 04958.0008-07000
CURRENT APPLICATION NUMBER: US/09/293,769A
CURRENT FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: 08/471,284
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 07/106,944
PRIOR FILING DATE: 1987-10-15
PRIOR APPLICATION NUMBER: EPO 92402326.0
PRIOR FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: EPO 93401310.3
PRIOR FILING DATE: 1993-05-21
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 109
LENGTH: 18
TYPE: PRT
ORGANISM: Camelus sp.
US-09-293-769A-109

Query Match 100.0%; Score 23; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 24

US-09-293-769A-110
Sequence 110, Application US/09293769A
Patent No. 6765087
GENERAL INFORMATION:
APPLICANT: CASTERMAN, CECILE
TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
FILE REFERENCE: 04958.0008-07000
CURRENT APPLICATION NUMBER: US/09/293,769A
CURRENT FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: 08/471,284
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 07/106,944
PRIOR FILING DATE: 1987-10-15
PRIOR APPLICATION NUMBER: EPO 92402326.0
PRIOR FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: EPO 93401310.3
PRIOR FILING DATE: 1993-05-21
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 110
LENGTH: 18
TYPE: PRT
ORGANISM: Camelus sp.
US-09-293-769A-110

Query Match 100.0%; Score 23; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 25

US-09-293-769A-111
Sequence 111, Application US/09293769A
Patent No. 6765087
GENERAL INFORMATION:
APPLICANT: CASTERMAN, CECILE
TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
FILE REFERENCE: 04958.0008-07000

CURRENT APPLICATION NUMBER: US/09/293,769A
CURRENT FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: 08/471,284
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 07/106,944
PRIOR FILING DATE: 1987-10-15
PRIOR APPLICATION NUMBER: EPO 92402326.0
PRIOR FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: EPO 93401310.3
PRIOR FILING DATE: 1993-05-21
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 111
LENGTH: 18
TYPE: PRT
ORGANISM: Camelus sp.
US-09-293-769A-111

Query Match 100.0%; Score 23; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 26

US-08-471-780C-115
Sequence 115, Application US/08471780C
Patent No. 5759808
GENERAL INFORMATION:
APPLICANT: CASTERMAN, Cecile
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,780C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-471-780C-115

Query Match 100.0%; Score 23; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 2 GQPR 5

RESULT 27

US-08-471-780C-116
 ; Sequence 116, Application US/08471780C
 ; Patent No. 5759808
 ; GENERAL INFORMATION:
 ; APPLICANT: Casterman, Cecile
 ; APPLICANT: Hamers, Raymond
 ; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
 ; NUMBER OF SEQUENCES: 130
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,780C
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/106,944
 FILING DATE: 17-AUG-1993
 APPLICATION NUMBER: FR 92402326.0
 FILING DATE: 21-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 93401310.3
 FILING DATE: 21-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Potter, Jane E.R.
 REGISTRATION NUMBER: 33,332
 REFERENCE/DOCKET NUMBER: 04958.0008-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 116:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-471-780C-116

Query Match 100.0%; Score 23; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 2 GQPR 5

RESULT 28

US-08-471-780C-117
 ; Sequence 117, Application US/08471780C
 ; Patent No. 5759808
 ; GENERAL INFORMATION:

APPLICANT: Casterman, Cecile
 APPLICANT: Hamers, Raymond
 TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
 NUMBER OF SEQUENCES: 130
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,780C
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/106,944
 FILING DATE: 17-AUG-1993
 APPLICATION NUMBER: FR 92402326.0
 FILING DATE: 21-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 93401310.3
 FILING DATE: 21-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Potter, Jane E.R.
 REGISTRATION NUMBER: 33,332
 REFERENCE/DOCKET NUMBER: 04958.0008-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 117:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-471-780C-117

Query Match 100.0%; Score 23; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db ||||
 2 GQPR 5

RESULT 29

US-08-467-282B-115
 ; Sequence 115, Application US/08467282B
 ; Patent No. 5800988
 ; GENERAL INFORMATION:
 ; APPLICANT: Casterman, Cecile
 ; APPLICANT: Hamers, Raymond
 ; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
 ; NUMBER OF SEQUENCES: 130
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/467,282B
;/ FILING DATE: 06-JUN-1995
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/106,944
;/ FILING DATE: 17-AUG-1993
;/ APPLICATION NUMBER: FR 92402326.0
;/ FILING DATE: 21-AUG-1992
;/ PRIOR APPLICATION DATA: FR 93401310.3
;/ FILING DATE: 21-MAY-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Potter, Jane E.R.
;/ REGISTRATION NUMBER: 33,332
;/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
;/ TELEPHONE: 202-408-4000
;/ TELEFAX: 202-408-4400
;/ INFORMATION FOR SEQ ID NO: 115:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 19 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-467-282B-115

Query Match 100.0%; Score 23; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db |||||
2 GQPR 5

RESULT 30
US-08-467-282B-116
;/ Sequence 116, Application US/08467282B
;/ Patent No. 5800988
;/ GENERAL INFORMATION:
;/ APPLICANT: Casterman, Cecile
;/ APPLICANT: Hamers, Raymond
;/ TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
;/ NUMBER OF SEQUENCES: 130
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;/ STREET: 1300 I Street, N.W.
;/ CITY: Washington
;/ STATE: D.C.
;/ COUNTRY: USA
;/ ZIP: 20005-3315
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/467,282B
;/ FILING DATE: 06-JUN-1995
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: FR 93401310.3
;/ FILING DATE: 21-MAY-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Potter, Jane E.R.
;/ REGISTRATION NUMBER: 33,332
;/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
;/ TELEPHONE: 202-408-4000
;/ TELEFAX: 202-408-4400
;/ INFORMATION FOR SEQ ID NO: 117:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 19 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-467-282B-117

Query Match 100.0%; Score 23; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db |||||
2 GQPR 5

;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-408-4000
;/ TELEFAX: 202-408-4400
;/ INFORMATION FOR SEQ ID NO: 116:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 19 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-467-282B-116

Query Match 100.0%; Score 23; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db |||||
2 GQPR 5

RESULT 31
US-08-467-282B-117
;/ Sequence 117, Application US/08467282B
;/ Patent No. 5800988
;/ GENERAL INFORMATION:
;/ APPLICANT: Casterman, Cecile
;/ APPLICANT: Hamers, Raymond
;/ TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
;/ NUMBER OF SEQUENCES: 130
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
;/ STREET: 1300 I Street, N.W.
;/ CITY: Washington
;/ STATE: D.C.
;/ COUNTRY: USA
;/ ZIP: 20005-3315
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/467,282B
;/ FILING DATE: 06-JUN-1995
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/106,944
;/ FILING DATE: 17-AUG-1993
;/ APPLICATION NUMBER: FR 92402326.0
;/ FILING DATE: 21-AUG-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: FR 93401310.3
;/ FILING DATE: 21-MAY-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Potter, Jane E.R.
;/ REGISTRATION NUMBER: 33,332
;/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-408-4000
;/ TELEFAX: 202-408-4400
;/ INFORMATION FOR SEQ ID NO: 117:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 19 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-467-282B-117

Query Match 100.0%; Score 23; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db |||||
2 GQPR 5

Db |||||
 2 GQPR 5

RESULT 32

US-08-471-282A-115
; Sequence 115, Application US/08471282A
; Patent No. 5840853
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,282A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-471-282A-115

Query Match 100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GQPR 4
 |||||
Db 2 GQPR 5

RESULT 33

US-08-471-282A-116
; Sequence 116, Application US/08471282A
; Patent No. 5840853
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.

; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,282A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-471-282A-116

Query Match 100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GQPR 4
 |||||
Db 2 GQPR 5

RESULT 34

US-08-471-282A-117
; Sequence 117, Application US/08471282A
; Patent No. 5840853
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,282A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993

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/ APPLICATION NUMBER: FR 92402326.0
/ FILING DATE: 21-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 93401310.3
/ FILING DATE: 21-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E.R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 117:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-471-282A-117

Query Match 100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
2 GQPR 5

RESULT 35
US-08-466-710C-115
/ Sequence 115, Application US/08466710C
/ Patent No. 5874541
/ GENERAL INFORMATION:
/ APPLICANT: Casterman, Cecile
/ APPLICANT: Hamers, Raymond
/ TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
/ NUMBER OF SEQUENCES: 130
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
/ STREET: 1300 I Street, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/466,710C
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/106,944
/ FILING DATE: 17-AUG-1993
/ APPLICATION NUMBER: FR 92402326.0
/ FILING DATE: 21-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 93401310.3
/ FILING DATE: 21-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E.R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 116:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-466-710C-116

Query Match 100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
2 GQPR 5

RESULT 36
US-08-466-710C-116
/ Sequence 116, Application US/08466710C
/ Patent No. 5874541
/ GENERAL INFORMATION:
/ APPLICANT: Casterman, Cecile
/ APPLICANT: Hamers, Raymond
/ TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
/ NUMBER OF SEQUENCES: 130
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
/ STREET: 1300 I Street, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/466,710C
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/106,944
/ FILING DATE: 17-AUG-1993
/ APPLICATION NUMBER: FR 92402326.0
/ FILING DATE: 21-AUG-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 93401310.3
/ FILING DATE: 21-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Potter, Jane E.R.
/ REGISTRATION NUMBER: 33,332
/ REFERENCE/DOCKET NUMBER: 04958.0008-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 116:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-466-710C-116

Query Match 100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
2 GQPR 5

RESULT 37
US-08-466-710C-117
/ Sequence 117, Application US/08466710C
```

```

; Patent No. 5874541
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,710C
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 117:
; FILING DATE: 21-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-466-710C-117

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```

Query Match 100.0%; Score 23; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 GQPR 4
Db 2 GQPR 5

```

```

RESULT 38
US-08-468-739C-115
; Sequence 115, Application US/08468739C
; Patent No. 6015695
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,739C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-468-739C-115

Query Match 100.0%; Score 23; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GQPR 4
Db 2 GQPR 5

RESULT 39
US-08-468-739C-116
; Sequence 116, Application US/08468739C
; Patent No. 6015695
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,739C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.

```

REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-739C-116

Query Match 100.0%; Score 23; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
2 GQPR 5

RESULT 40

US-08-468-739C-117
Sequence 117, Application US/08468739C
Patent No. 6015695
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,739C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944

FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.

REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-739C-117

Query Match 100.0%; Score 23; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
2 GQPR 5

RESULT 41

US-09-293-769A-115
Sequence 115, Application US/09293769A
Patent No. 6765087
GENERAL INFORMATION:
APPLICANT: CASTERMAN, CECILE
APPLICANT: HAMERS, RAYMOND
TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
FILE REFERENCE: 04958.0008-07000
CURRENT APPLICATION NUMBER: US/09/293,769A
CURRENT FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: 08/471,284
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 07/106,944
PRIOR FILING DATE: 1987-10-15
PRIOR APPLICATION NUMBER: EPO 92402326.0
PRIOR FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: EPO 93401310.3
PRIOR FILING DATE: 1993-05-21
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 115
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-09-293-769A-115

Query Match 100.0%; Score 23; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db ||||
2 GQPR 5

RESULT 42

US-09-293-769A-116
Sequence 116, Application US/09293769A
Patent No. 6765087
GENERAL INFORMATION:
APPLICANT: CASTERMAN, CECILE
APPLICANT: HAMERS, RAYMOND
TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
FILE REFERENCE: 04958.0008-07000
CURRENT APPLICATION NUMBER: US/09/293,769A
CURRENT FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: 08/471,284
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 07/106,944
PRIOR FILING DATE: 1987-10-15
PRIOR APPLICATION NUMBER: EPO 92402326.0
PRIOR FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: EPO 93401310.3
PRIOR FILING DATE: 1993-05-21
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 116
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-09-293-769A-116

Query Match 100.0%; Score 23; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOPR 4
Db 2 QOPR 5

RESULT 43

US-09-293-769A-117
; Sequence 117, Application US/09293769A
; Patent No. 6765087

GENERAL INFORMATION:

; APPLICANT: CASTERMAN, CECILE
; APPLICANT: HAMERS, RAYMOND
; TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
; FILE REFERENCE: 04958.0008-07000
; CURRENT APPLICATION NUMBER: US/09/293,769A
; CURRENT FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: 08/471,284
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/106,944
; PRIOR FILING DATE: 1987-10-15
; PRIOR APPLICATION NUMBER: EPO 92402326.0
; PRIOR FILING DATE: 1992-08-21
; PRIOR APPLICATION NUMBER: EPO 93401310.3
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-293-769A-117

Query Match 100.0%; Score 23; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOPR 4
Db 2 QOPR 5

RESULT 44

US-08-851-843A-194
; Sequence 194, Application US/08851843A
; Patent No. 6093809

GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843A
; FILING DATE: 06-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-851-843A-194

Query Match 100.0%; Score 23; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOPR 4
Db 15 QOPR 18

RESULT 45

US-08-974-549A-313
; Sequence 313, Application US/08974549A
; Patent No. 6166178

GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017

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; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA: US 08/851,843
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 313:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-549A-313

Query Match 100.0%; Score 23; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 15 GQPR 18

RESULT 46
US-08-854-050-194
; Sequence 194, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA: US 08/851,843
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-854-050-194

Query Match 100.0%; Score 23; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 15 GQPR 18

RESULT 47
US-09-430-323-194
; Sequence 194, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
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;
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-430-323-194

Query Match 100.0%; Score 23; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 15 GQPR 18

RESULT 48
US-09-402-181B-313
; Sequence 313, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419

;
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 313:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 313:
US-09-402-181B-313

Query Match 100.0%; Score 23; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 15 GQPR 18

RESULT 49
US-09-721-456-313
; Sequence 313, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-No. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 313:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 313:
US-09-721-456-313

Query Match 100.0%; Score 23; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 GQPR 4
Db 15 GQPR 18

RESULT 50
US-08-708-893-1
Sequence 1, Application US/08708893
Patent No. 5760175
GENERAL INFORMATION:
APPLICANT: Golubev, Daniel B
APPLICANT: Chaihorsky, Alexander
TITLE OF INVENTION: PEPTIDE VACCINE TO PREVENT DEVELOPMENT OF
TITLE OF INVENTION: SEVERAL HERPES VIRUS INFECTIONS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Firm of Karl F. Ross, PC
STREET: 5676 Riverdale Ave.
CITY: Bronx
STATE: New York
COUNTRY: USA
ZIP: 10471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/708,893
FILING DATE:
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Jonathan E
REGISTRATION NUMBER: 26,963
REFERENCE/DOCKET NUMBER: 20075
TELEPHONE: (718) 884-6600
TELEFAX: 718/601-1099
TELEX: 620428
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-708-893-1
Query Match 100.0%; Score 23; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 GQPR 4
Db 24 GQPR 27

RESULT 51
US-09-088-154-1
Sequence 1, Application US/09088154
Patent No. 6015566
GENERAL INFORMATION:
APPLICANT: Golubev, Daniel B
APPLICANT: Chaihorsky, Alexander
TITLE OF INVENTION: PEPTIDE VACCINE TO PREVENT DEVELOPMENT OF
TITLE OF INVENTION: SEVERAL HERPES VIRUS INFECTIONS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Firm of Karl F. Ross, PC
STREET: 5676 Riverdale Ave.
CITY: Bronx
STATE: New York
COUNTRY: USA
ZIP: 10471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,154
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/708,893
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Jonathan E
REGISTRATION NUMBER: 26,963
REFERENCE/DOCKET NUMBER: 20075
TELEPHONE: (718) 884-6600
TELEFAX: 718/601-1099
TELEX: 620428
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO


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; ANTI-SENSE: NO
US-09-088-154-1
Query Match      100.0%; Score 23; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      24 GQPR 27

RESULT 52
US-08-809-440-16
; Sequence 16, Application US/08809440
; Patent No. 5929017
; GENERAL INFORMATION:
; APPLICANT: Gormsen, Erik
; APPLICANT: Ikegami, Naoko
; APPLICANT: Abo, Masanobu
; APPLICANT: Takagi, Shinobu
; APPLICANT: Tsutsumi, No. 5929017iko
; APPLICANT: Halkier, Torben
; TITLE OF INVENTION: Enzymatic Detergent Composition
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5929017o No. 5929017disk of No. 5929017th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,440
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris, Cheryl H
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4295.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5929017e
US-08-809-440-16

Query Match      100.0%; Score 23; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      18 GQPR 21

RESULT 53
US-09-523-686-2
; Sequence 2, Application US/09523686
; Patent No. 6518043
; GENERAL INFORMATION:
; APPLICANT: Oritani, Kenji
```

```
; APPLICANT: Tomiyama, Yoshiaki
; APPLICANT: Matsuzawa, Yuji
; APPLICANT: Paul W. Kincade
; TITLE OF INVENTION: Proteins Suppressing proliferation of lympho-hematopoietic cells
; FILE REFERENCE: SEN-103-US
; CURRENT APPLICATION NUMBER: US/09/523,686
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: JP 1999-107246
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-523-686-2

Query Match      100.0%; Score 23; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      13 GQPR 16

RESULT 54
US-10-038-612-70
; Sequence 70, Application US/10038612
; Patent No. 6723830
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: Short peptides which selectively
; TITLE OF INVENTION: Modulate the Activity of Protein Kinases
; FILE REFERENCE: 1242.1029-000 (CMCC-679)
; CURRENT APPLICATION NUMBER: US/10/038,612
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 35
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: TrkC
US-10-038-612-70

Query Match      100.0%; Score 23; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      26 GQPR 29

RESULT 55
US-09-461-325-262
; Sequence 262, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: PZ029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
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; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 262
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-325-262

Query Match      100.0%; Score 23; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      16 GQPR 19

RESULT 56
US-10-012-542-262
; Sequence 262, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: PZ029PI
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 262
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-542-262

Query Match      100.0%; Score 23; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      16 GQPR 19

RESULT 57
US-10-115-123-262
; Sequence 262, Application US/10115123
; Patent No. 6774216
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
```

```
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: PZ029G30AP1D2
; CURRENT APPLICATION NUMBER: US/10/115,123
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 262
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-123-262

Query Match      100.0%; Score 23; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      16 GQPR 19

RESULT 58
US-08-809-440-15
; Sequence 15, Application US/08809440
; Patent No. 5929017
; GENERAL INFORMATION:
; APPLICANT: Gormsen, Erik
; APPLICANT: Ikegami, Naoko
; APPLICANT: Abo, Masanobu
; APPLICANT: Takagi, Shinobu
; APPLICANT: Tsutsumi, No. 5929017iko
; APPLICANT: Haikier, Torben
; TITLE OF INVENTION: Enzymatic Detergent Composition
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSES: No. 5929017o No. 5929017disk of No. 5929017th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,440
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Agis, Cheryl H
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4295.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. 5929017e
US-08-809-440-15

Query Match 100.0%; Score 23; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
    ||||
Db 34 GQPR 37

RESULT 59
US-08-548-540-94
; Sequence 94, Application US/08548540
; Patent No. 5733731
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Gates, Christian M.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09809
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,540
; FILING DATE: 26-OCT-1995
; APPLICATION NUMBER: US 08/290,641
; FILING DATE: 15-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,321
; FILING DATE: 15-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528J-001240US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US96-09809-94

Query Match 100.0%; Score 23; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
    ||||
Db 25 GQPR 28

RESULT 61
US-08-488-161-66
; Sequence 66, Application US/08488161
; Patent No. 5865577
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Vernon L.
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; TITLE OF INVENTION: Peptide Libraries
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:
; STREET:
; CITY:
; STATE:
; COUNTRY:
; ZIP:
; COMPUTER READABLE FORM:
; MEDIUM TYPE:
; COMPUTER:
; OPERATING SYSTEM:
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH:
; TYPE:
; STRANDEDNESS:
; TOPOLOGY:
; MOLECULE TYPE:
; PCT-US96-09809-94

Query Match 100.0%; Score 23; DB 5; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
    ||||
Db 25 GQPR 28

RESULT 61
US-08-488-161-66
; Sequence 66, Application US/08488161
; Patent No. 5865577
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Vernon L.
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; TITLE OF INVENTION: Peptide Libraries
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-176
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-161-66

Query Match 100.0%; Score 23; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 7 GQPR 10

RESULT 62
US-09-273-685-66
Sequence 66, Application US/09273685
Patent No. 6015561
GENERAL INFORMATION:
APPLICANT: Alvarez, Vernon L.
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
REFERENCE/DOCKET NUMBER: 1101-176
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/488,161
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-176

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-273-685-66

Query Match 100.0%; Score 23; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 7 GQPR 10

RESULT 63
PCT-US95-11934-66
Sequence 66, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
REFERENCE/DOCKET NUMBER: 1101-196-228
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-11934-66

Query Match 100.0%; Score 23; DB 5; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 7 GQPR 10

RESULT 64

US-08-548-540-93
; Sequence 93, Application US/08548540
; Patent No. 5733731
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Gates, Christian M.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/548,540
; FILING DATE: 26-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/290,641
; FILING DATE: 15-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,321
; FILING DATE: 15-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528J-001240US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-548-540-93
Query Match 100.0%; Score 23; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 26 GQPR 29
RESULT 65
PCT-US96-09809-93
; Sequence 93, Application PC/TUS9609809
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Gates, Christian M.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09809
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,540
FILING DATE: 26-OCT-1995
APPLICATION NUMBER: US 08/290,641
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528J-001240US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-09809-93
Query Match 100.0%; Score 23; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 26 GQPR 29
RESULT 66
US-08-809-440-17
; Sequence 17, Application US/08809440
; Patent No. 5929017
; GENERAL INFORMATION:
; APPLICANT: Gormsen, Erik
; APPLICANT: Ikegami, Naoko
; APPLICANT: Abo, Masanobu
; APPLICANT: Takagi, Shinobu
; APPLICANT: Teutsumi, No. 5929017iko
; APPLICANT: Halkier, Torben
; TITLE OF INVENTION: Enzymatic Detergent Composition
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5929017o.No. 5929017disk of No. 5929017th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,440
; FILING DATE: 24-APR-1997

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; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Agtis, Cheryl H
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4295.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5929017e
US-08-809-440-17

Query Match 100.0%; Score 23; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 34 GQPR 37

RESULT 67
US-09-434-840-65
; Sequence 65, Application US/09434840
; Patent No. 6620985
; GENERAL INFORMATION:
; APPLICANT: Glazebrook, Jane
; APPLICANT: Jirage, Dayadevi
; APPLICANT: Tootle, Tina L
; APPLICANT: Zhou, Nan
; APPLICANT: Feys, Bart
; TITLE OF INVENTION: PAD4 COMPOSITIONS AND METHODS THEREFOR
; FILE REFERENCE: 043503.0009
; CURRENT APPLICATION NUMBER: US/09/434,840
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: 09/190,733
; EARLIER FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Rhizomucor miehei
US-09-434-840-65

Query Match 100.0%; Score 23; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 20 GQPR 23

RESULT 68
US-09-270-767-42207
; Sequence 42207, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42207
```

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; LENGTH: 55
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-42207

Query Match 100.0%; Score 23; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 32 GQPR 35

RESULT 69
US-09-270-767-60731
; Sequence 60731, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60731
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-60731

Query Match 100.0%; Score 23; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 25 GQPR 28

RESULT 70
US-09-489-039A-8043
; Sequence 8043, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8043
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8043

Query Match 100.0%; Score 23; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 21 GQPR 24

RESULT 71
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US-09-248-796A-27059
; Sequence 27059, Application US/09248796A
; Patent No. 6747137

GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 27059

; LENGTH: 60
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-27059

Query Match 100.0%; Score 23; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 48 GQPR 51

RESULT 72

US-08-754-477A-139
; Sequence 139, Application US/08754477A
; Patent No. 6518411

GENERAL INFORMATION:

; APPLICANT: Murray, Jeffrey
; APPLICANT: Semina, Elena
; TITLE OF INVENTION: RIEG COMPOSITIONS AND THERAPEUTIC
; TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/754,477A
; FILING DATE: 22-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430

; REFERENCE/DOCKET NUMBER: UIA-022.01

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 139:

SEQUENCE CHARACTERISTICS:

; LENGTH: 68 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-754-477A-139

Query Match 100.0%; Score 23; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 42 GQPR 45

RESULT 73

US-09-227-357-163
; Sequence 163, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.

; TITLE OF INVENTION: 123 Human Secreted Proteins

; FILE REFERENCE: P2010P1

; CURRENT APPLICATION NUMBER: US/09/227,357

; CURRENT FILING DATE: 1999-01-08

; EARLIER APPLICATION NUMBER: PCT/US98/13684

; EARLIER FILING DATE: 1998-07-07

; EARLIER APPLICATION NUMBER: 60/051,926

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/052,793

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,925

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,929

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/052,803

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/052,732

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,931

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,932

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,916

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,930

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,918

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,920

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/052,733

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/052,795

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,919

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,928

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/055,722

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,723

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,948

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,949

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,953

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,950

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,947

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,964

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/056,360

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,684

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,984

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,954

; EARLIER FILING DATE: 1997-08-18

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; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (51)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-227-357-163

Query Match      100.0%; Score 23; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      55 GQPR 58

RESULT 74
US-09-270-767-32321
; Sequence 32321, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32321
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32321

Query Match      100.0%; Score 23; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      48 GQPR 51

RESULT 75
US-09-270-767-47538
; Sequence 47538, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47538
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Drosophila melanogaster

US-09-270-767-47538
Query Match      100.0%; Score 23; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      48 GQPR 51

Search completed: May 17, 2005, 10:08:24
Job time : 34 secs
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Result No.	Score	Query ϵ			ID	Description
		Match	Length	DB		
1	23	100.0	4	14	US-10-197-954-120	Sequence 120, App
2	23	100.0	4	16	US-10-742-344-3	Sequence 3, Appli
3	23	100.0	4	16	US-10-731-921-3	Sequence 3, Appli
4	23	100.0	4	17	US-10-760-085-120	Sequence 120, App
5	23	100.0	9	9	US-09-776-874A-8	Sequence 8, Appli
6	23	100.0	9	9	US-09-988-113-8	Sequence 8, Appli
7	23	100.0	9	14	US-10-341-582-8	Sequence 8, Appli
8	23	100.0	9	14	US-10-384-451-8	Sequence 8, Appli
9	23	100.0	9	14	US-10-384-450-8	Sequence 8, Appli
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11	23	100.0	9	15	US-10-456-573-8	Sequence 8, Appli
12	23	100.0	9	16	US-10-785-116-8	Sequence 8, Appli
13	23	100.0	12	11	US-09-920-106-63	Sequence 63, Appli

87	23	100.0	74	11	US-09-833-245-2128	Sequence 2128, Ap	160	23	100.0	100	16	US-10-437-963-147030	Sequence 147030,
88	23	100.0	74	11	US-09-973-278-206	Sequence 206, App	161	23	100.0	100	16	US-10-437-963-160978	Sequence 160978,
89	23	100.0	74	14	US-10-029-386-28857	Sequence 28857, A	162	23	100.0	100	16	US-10-437-963-162749	Sequence 162749,
90	23	100.0	74	16	US-10-437-963-140587	Sequence 140587,	163	23	100.0	100	16	US-10-437-963-172248	Sequence 172248,
91	23	100.0	74	16	US-10-437-963-173930	Sequence 173930,	164	23	100.0	101	16	US-10-437-963-138801	Sequence 138801,
92	23	100.0	74	16	US-10-437-963-196719	Sequence 196719,	165	23	100.0	102	15	US-10-104-047-3923	Sequence 3923, Ap
93	23	100.0	74	17	US-10-883-936-124	Sequence 124, App	166	23	100.0	102	15	US-10-424-599-143920	Sequence 143920,
94	23	100.0	75	15	US-10-424-599-156672	Sequence 156672,	167	23	100.0	102	15	US-10-424-599-154941	Sequence 154941,
95	23	100.0	75	15	US-10-425-114-70336	Sequence 70336, A	168	23	100.0	102	15	US-10-424-599-194109	Sequence 194109,
96	23	100.0	75	16	US-10-437-963-152229	Sequence 152229,	169	23	100.0	102	15	US-10-424-599-216941	Sequence 216941,
97	23	100.0	75	16	US-10-437-963-171622	Sequence 171622,	170	23	100.0	102	15	US-10-424-599-240595	Sequence 240595,
98	23	100.0	75	16	US-10-437-963-172136	Sequence 172136,	171	23	100.0	103	15	US-10-424-599-231032	Sequence 231032,
99	23	100.0	76	15	US-10-424-599-236220	Sequence 236220,	172	23	100.0	103	16	US-10-437-963-121650	Sequence 121650,
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102	23	100.0	77	11	US-09-864-408A-6800	Sequence 6800, Ap	175	23	100.0	105	16	US-10-437-963-155376	Sequence 155376,
103	23	100.0	78	16	US-10-437-963-145755	Sequence 145755,	176	23	100.0	105	16	US-10-437-963-163883	Sequence 163883,
104	23	100.0	78	16	US-10-437-963-183354	Sequence 183354,	177	23	100.0	106	15	US-10-424-599-188365	Sequence 188365,
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106	23	100.0	79	15	US-10-424-599-179326	Sequence 179326,	179	23	100.0	106	16	US-10-437-963-164863	Sequence 164863,
107	23	100.0	80	16	US-10-437-963-145218	Sequence 145218,	180	23	100.0	107	14	US-10-267-286A-5	Sequence 5, Appli
108	23	100.0	80	16	US-10-437-963-169341	Sequence 169341,	181	23	100.0	107	14	US-10-207-655-222	Sequence 222, App
109	23	100.0	80	16	US-10-437-963-173391	Sequence 173391,	182	23	100.0	107	14	US-10-207-655-375	Sequence 375, App
110	23	100.0	80	16	US-10-767-701-54726	Sequence 54726, A	183	23	100.0	107	14	US-10-207-655-376	Sequence 376, App
111	23	100.0	81	15	US-10-424-599-148176	Sequence 148176,	184	23	100.0	107	14	US-10-207-655-377	Sequence 377, App
112	23	100.0	81	15	US-10-424-599-234140	Sequence 234140,	185	23	100.0	107	14	US-10-207-655-378	Sequence 378, App
113	23	100.0	82	11	US-09-833-245-136	Sequence 196, App	186	23	100.0	107	14	US-10-207-655-379	Sequence 379, App
114	23	100.0	82	14	US-10-029-386-28922	Sequence 28922, A	187	23	100.0	107	15	US-10-370-749-24	Sequence 24, Appl
115	23	100.0	82	15	US-10-424-599-191577	Sequence 191577,	188	23	100.0	107	15	US-10-264-049-2368	Sequence 2368, Ap
116	23	100.0	82	15	US-10-425-000-93	Sequence 93, Appl	189	23	100.0	107	15	US-10-424-599-208487	Sequence 208487,
117	23	100.0	82	15	US-10-424-999-58	Sequence 58, Appl	190	23	100.0	107	15	US-10-425-114-40171	Sequence 40171, A
118	23	100.0	82	16	US-10-767-701-42420	Sequence 42420, A	191	23	100.0	107	16	US-10-307-276B-46	Sequence 46, Appl
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120	23	100.0	83	15	US-10-424-599-208799	Sequence 208799,	193	23	100.0	107	16	US-10-437-963-108177	Sequence 108177,
121	23	100.0	84	16	US-10-437-963-164940	Sequence 164940,	194	23	100.0	107	16	US-10-437-963-134747	Sequence 134747,
122	23	100.0	85	15	US-10-424-599-247618	Sequence 247618,	195	23	100.0	107	16	US-10-684-109-74	Sequence 74, Appl
123	23	100.0	86	10	US-09-764-872-407	Sequence 407, App	196	23	100.0	107	17	US-10-491-653-6	Sequence 6, Appli
124	23	100.0	86	16	US-10-767-701-32827	Sequence 32827, A	197	23	100.0	108	9	US-09-864-761-42141	Sequence 42141, A
125	23	100.0	87	9	US-09-867-550-1118	Sequence 1118, Ap	198	23	100.0	108	14	US-10-020-354-81	Sequence 81, Appl
126	23	100.0	87	9	US-09-764-868-1134	Sequence 1134, Ap	199	23	100.0	108	15	US-10-424-599-251295	Sequence 251295,
127	23	100.0	87	11	US-09-764-875-983	Sequence 983, App	200	23	100.0	108	16	US-10-437-963-177036	Sequence 177036,
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129	23	100.0	88	9	US-09-864-761-36851	Sequence 36851, A	202	23	100.0	109	15	US-10-425-114-47617	Sequence 47617, A
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131	23	100.0	89	15	US-10-424-599-173264	Sequence 173264,	204	23	100.0	109	16	US-10-437-963-155116	Sequence 155116,
132	23	100.0	89	16	US-10-408-765A-780	Sequence 780, App	205	23	100.0	109	16	US-10-437-963-177648	Sequence 177648,
133	23	100.0	89	16	US-10-408-765A-781	Sequence 781, App	206	23	100.0	110	14	US-10-029-386-29859	Sequence 29859, A
134	23	100.0	89	16	US-10-437-963-137032	Sequence 137032,	207	23	100.0	110	15	US-10-424-599-260983	Sequence 260983,
135	23	100.0	89	17	US-10-874-706-11	Sequence 11, Appl	208	23	100.0	110	16	US-10-437-963-198752	Sequence 198752,
136	23	100.0	90	16	US-10-437-963-169859	Sequence 169859,	209	23	100.0	111	15	US-10-112-944-813	Sequence 813, App
137	23	100.0	90	16	US-10-437-963-176549	Sequence 176549,	210	23	100.0	111	16	US-10-767-701-32670	Sequence 32670, A
138	23	100.0	91	9	US-09-814-777A-7	Sequence 7, Appli	211	23	100.0	112	15	US-10-424-599-145079	Sequence 145079,
139	23	100.0	92	14	US-10-106-698-8371	Sequence 8371, Ap	212	23	100.0	112	15	US-10-424-599-165610	Sequence 165610,
140	23	100.0	92	16	US-10-437-963-123359	Sequence 123359,	213	23	100.0	113	15	US-09-922-226-129	Sequence 129, App
141	23	100.0	93	16	US-10-437-963-138163	Sequence 138163,	214	23	100.0	113	14	US-10-029-386-31331	Sequence 31331, A
142	23	100.0	93	16	US-10-767-701-36878	Sequence 36878, A	215	23	100.0	113	15	US-10-424-599-171969	Sequence 171969,
143	23	100.0	94	15	US-10-264-049-2545	Sequence 2545, Ap	216	23	100.0	113	16	US-10-437-963-125572	Sequence 125572,
144	23	100.0	94	16	US-10-437-963-107682	Sequence 107682,	217	23	100.0	114	9	US-09-864-761-42278	Sequence 42278, A
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147	23	100.0	96	15	US-10-243-552-456	Sequence 456, App	220	23	100.0	115	15	US-10-094-749-2764	Sequence 2764, Ap
148	23	100.0	96	15	US-10-424-599-191513	Sequence 191513,	221	23	100.0	115	15	US-10-424-599-223544	Sequence 223544,
149	23	100.0	96	16	US-10-437-963-140221	Sequence 140221,	222	23	100.0	115	15	US-10-425-114-48965	Sequence 48965, A
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153	23	100.0	98	15	US-10-424-599-270892	Sequence 270892,	226	23	100.0	118	15	US-10-424-599-171957	Sequence 171957,
154	23	100.0	98	15	US-10-425-114-60729	Sequence 60729, A	227	23	100.0	118	16	US-10-437-963-138829	Sequence 138829,
155	23	100.0	98	16	US-10-437-963-196738	Sequence 196738,	228	23	100.0	118	16	US-10-437-963-202851	Sequence 202851,
156	23	100.0	98	16	US-10-767-701-53395	Sequence 53395, A	229	23	100.0	119	16	US-10-437-963-103120	Sequence 103120,
157	23	100.0	99	16	US-10-437-963-141929	Sequence 141929,	230	23	100.0	119	16	US-10-437-963-127851	Sequence 127851,
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159	23	100.0	100	16	US-10-437-963-138859	Sequence 138859,	232	23	100.0	120	16	US-10-437-963-163722	Sequence 163722,

233	23	100.0	120	16	US-10-767-701-46585	Sequence 46585, A	306	23	100.0	148	16	US-10-437-963-114731	Sequence 114731, A
234	23	100.0	120	16	US-10-767-701-53752	Sequence 53752, A	307	23	100.0	149	9	US-09-764-847-517	Sequence 517, App
235	23	100.0	121	16	US-10-437-963-131318	Sequence 131318, A	308	23	100.0	149	14	US-10-092-154-517	Sequence 32381, A
236	23	100.0	121	16	US-10-437-963-140181	Sequence 140181, A	309	23	100.0	150	16	US-10-767-701-32381	Sequence 32381, A
237	23	100.0	121	16	US-09-925-299-1161	Sequence 1161, App	310	23	100.0	150	16	US-10-767-701-37105	Sequence 37105, A
238	23	100.0	123	9	US-09-925-299-1161	Sequence 1161, App	311	23	100.0	150	16	US-10-767-701-44536	Sequence 44536, A
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240	23	100.0	124	16	US-10-437-963-176651	Sequence 176651, A	313	23	100.0	151	16	US-10-437-963-115199	Sequence 115199, A
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242	23	100.0	125	16	US-10-437-963-189234	Sequence 189234, A	315	23	100.0	152	9	US-09-864-761-37742	Sequence 37742, A
243	23	100.0	126	14	US-10-277-726A-15	Sequence 15, App	316	23	100.0	152	14	US-10-029-386-32515	Sequence 32515, A
244	23	100.0	126	15	US-10-425-114-50397	Sequence 50397, A	317	23	100.0	152	16	US-10-437-963-131079	Sequence 131079, A
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248	23	100.0	127	15	US-10-424-599-254333	Sequence 254333, A	321	23	100.0	153	15	US-10-296-115-1374	Sequence 1374, App
249	23	100.0	127	15	US-10-425-114-62773	Sequence 62773, A	322	23	100.0	153	16	US-10-437-963-120683	Sequence 120683, A
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253	23	100.0	128	16	US-10-437-963-178556	Sequence 178556, A	326	23	100.0	155	15	US-10-424-599-153610	Sequence 153610, A
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257	23	100.0	129	16	US-10-080-170-492	Sequence 492, App	330	23	100.0	156	16	US-10-437-963-127387	Sequence 127387, A
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260	23	100.0	130	15	US-10-276-774-1582	Sequence 1582, App	333	23	100.0	157	16	US-10-767-701-35001	Sequence 35001, A
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262	23	100.0	131	16	US-10-767-701-62321	Sequence 62321, A	335	23	100.0	158	9	US-09-864-761-35338	Sequence 35338, A
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266	23	100.0	133	15	US-10-369-493-3331	Sequence 3331, App	339	23	100.0	159	15	US-10-424-599-284164	Sequence 284164, A
267	23	100.0	133	16	US-10-437-963-122495	Sequence 122495, A	340	23	100.0	160	9	US-09-321-801-17	Sequence 17, Appl
268	23	100.0	134	8	US-08-424-550B-189	Sequence 189, App	341	23	100.0	160	15	US-10-369-493-12589	Sequence 12589, A
269	23	100.0	134	15	US-10-425-114-49753	Sequence 49753, A	342	23	100.0	161	15	US-10-618-252-17	Sequence 17, Appl
270	23	100.0	135	15	US-10-104-047-2220	Sequence 2220, App	343	23	100.0	161	14	US-10-029-386-23046	Sequence 23046, A
271	23	100.0	136	15	US-10-424-599-235397	Sequence 235397, A	344	23	100.0	161	15	US-10-425-114-41096	Sequence 41096, A
272	23	100.0	137	14	US-10-156-761-9022	Sequence 9022, App	345	23	100.0	161	15	US-10-425-114-53079	Sequence 53079, A
273	23	100.0	137	15	US-10-424-599-160562	Sequence 160562, A	346	23	100.0	162	15	US-10-104-047-2150	Sequence 2150, App
274	23	100.0	137	15	US-10-425-114-48496	Sequence 48496, A	347	23	100.0	162	15	US-10-264-237-1761	Sequence 1761, App
275	23	100.0	137	15	US-10-425-114-56171	Sequence 56171, A	348	23	100.0	162	15	US-10-424-599-146656	Sequence 146656, A
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279	23	100.0	139	15	US-10-264-237-2671	Sequence 2671, App	352	23	100.0	163	15	US-10-282-132A-59917	Sequence 59917, A
280	23	100.0	139	16	US-10-408-785A-2222	Sequence 2222, App	353	23	100.0	163	15	US-10-425-114-48880	Sequence 48880, A
281	23	100.0	140	13	US-10-077-438-5	Sequence 5, Appl	354	23	100.0	163	16	US-10-437-963-158525	Sequence 158525, A
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285	23	100.0	141	10	US-09-305-736-477	Sequence 477, App	358	23	100.0	165	17	US-10-726-332-2	Sequence 2, Appl
286	23	100.0	141	10	US-09-818-683-477	Sequence 477, App	359	23	100.0	166	9	US-09-864-761-37883	Sequence 37883, A
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289	23	100.0	141	15	US-10-621-401-476	Sequence 476, App	362	23	100.0	166	16	US-10-437-963-151442	Sequence 151442, A
290	23	100.0	142	16	US-10-437-963-141796	Sequence 141796, A	363	23	100.0	167	9	US-09-925-299-803	Sequence 803, App
291	23	100.0	142	16	US-10-437-963-172454	Sequence 172454, A	364	23	100.0	167	10	US-09-925-299-803	Sequence 803, App
292	23	100.0	142	16	US-10-437-963-202350	Sequence 202350, A	365	23	100.0	167	14	US-10-029-386-28584	Sequence 28584, A
293	23	100.0	143	15	US-10-264-049-3639	Sequence 3639, App	366	23	100.0	167	16	US-10-437-963-167228	Sequence 167228, A
294	23	100.0	143	15	US-10-424-599-175647	Sequence 175647, A	367	23	100.0	167	16	US-10-437-963-191594	Sequence 191594, A
295	23	100.0	145	9	US-09-854-286-6	Sequence 6, Appl	368	23	100.0	167	16	US-10-767-701-58779	Sequence 58779, A
296	23	100.0	146	15	US-10-424-599-154780	Sequence 154780, A	369	23	100.0	168	15	US-10-094-749-1743	Sequence 1743, App
297	23	100.0	146	15	US-10-424-599-192251	Sequence 192251, A	370	23	100.0	168	15	US-10-424-599-232991	Sequence 232991, A
298	23	100.0	146	16	US-10-437-963-113820	Sequence 113820, A	371	23	100.0	168	15	US-10-425-114-47490	Sequence 47490, A
299	23	100.0	146	16	US-10-767-701-61987	Sequence 61987, A	372	23	100.0	168	15	US-10-425-114-68577	Sequence 68577, A
300	23	100.0	147	15	US-10-264-237-1946	Sequence 1946, App	373	23	100.0	168	17	US-10-487-078-33	Sequence 33, Appl
301	23	100.0	147	15	US-10-264-237-2088	Sequence 2088, App	374	23	100.0	169	15	US-10-424-599-146090	Sequence 146090, A
302	23	100.0	147	15	US-10-425-114-50858	Sequence 50858, A	375	23	100.0	170	15	US-10-424-599-168814	Sequence 168814, A
303	23	100.0	147	15	US-10-363-616-472	Sequence 472, App	376	23	100.0	170	15	US-10-425-114-67066	Sequence 67066, A
304	23	100.0	147	16	US-10-437-963-135958	Sequence 135958, A	377	23	100.0	172	16	US-10-767-701-60162	Sequence 60162, A
305	23	100.0	148	15	US-10-425-114-71163	Sequence 71163, A	378	23	100.0	173	15	US-10-424-599-171397	Sequence 171397, A

379	23	100.0	175	9	US-09-854-280-23	Sequence 23, Appl	452	23	100.0	180	14	US-10-121-050-446	Sequence 446, App
380	23	100.0	175	9	US-09-854-208-23	Sequence 23, Appl	453	23	100.0	180	14	US-10-141-755-446	Sequence 446, App
381	23	100.0	175	16	US-10-767-701-40803	Sequence 40803, A	454	23	100.0	180	14	US-10-167-749-470	Sequence 470, App
382	23	100.0	176	15	US-10-425-114-3248	Sequence 39248, A	455	23	100.0	180	14	US-10-143-032-446	Sequence 446, App
383	23	100.0	177	15	US-09-793-932-95	Sequence 95, Appl	456	23	100.0	180	14	US-10-013-921A-470	Sequence 470, App
384	23	100.0	177	15	US-10-424-599-221369	Sequence 221369, A	457	23	100.0	180	14	US-10-123-108-446	Sequence 446, App
385	23	100.0	178	14	US-10-375-876-4	Sequence 9896, Ap	458	23	100.0	180	14	US-10-123-236-446	Sequence 446, App
386	23	100.0	178	14	US-10-375-876-4	Sequence 4, Appli	459	23	100.0	180	14	US-10-123-261-446	Sequence 446, App
387	23	100.0	178	15	US-10-214-545-4	Sequence 4, Appli	460	23	100.0	180	14	US-10-140-921-446	Sequence 446, App
388	23	100.0	178	15	US-10-215-545-4	Sequence 4, Appli	461	23	100.0	180	14	US-10-140-928-446	Sequence 446, App
389	23	100.0	178	16	US-10-437-963-150244	Sequence 150244, A	462	23	100.0	180	14	US-10-013-929A-470	Sequence 470, App
390	23	100.0	179	15	US-10-425-114-65557	Sequence 65557, A	463	23	100.0	180	14	US-10-016-177A-470	Sequence 470, App
391	23	100.0	179	16	US-10-767-701-35404	Sequence 35404, A	464	23	100.0	180	14	US-10-121-045-446	Sequence 446, App
392	23	100.0	180	9	US-09-731-816-8	Sequence 8, Appli	465	23	100.0	180	14	US-10-123-292-446	Sequence 446, App
393	23	100.0	180	9	US-09-794-705A-2	Sequence 2, Appli	466	23	100.0	180	14	US-10-123-903-446	Sequence 446, App
394	23	100.0	180	9	US-09-854-280-1	Sequence 1, Appli	467	23	100.0	180	14	US-10-124-819-446	Sequence 446, App
395	23	100.0	180	9	US-09-854-208-1	Sequence 1, Appli	468	23	100.0	180	14	US-10-124-822-446	Sequence 446, App
396	23	100.0	180	9	US-09-978-295A-470	Sequence 470, App	469	23	100.0	180	14	US-10-140-925-446	Sequence 446, App
397	23	100.0	180	9	US-09-978-697-470	Sequence 470, App	470	23	100.0	180	14	US-10-160-498-446	Sequence 446, App
398	23	100.0	180	9	US-09-874-503-2	Sequence 2, Appli	471	23	100.0	180	14	US-10-124-824-446	Sequence 446, App
399	23	100.0	180	9	US-09-978-192A-470	Sequence 470, App	472	23	100.0	180	14	US-10-127-825A-446	Sequence 446, App
400	23	100.0	180	9	US-09-999-832A-470	Sequence 470, App	473	23	100.0	180	14	US-10-127-829A-446	Sequence 446, App
401	23	100.0	180	10	US-09-320-713-8	Sequence 8, Appli	474	23	100.0	180	14	US-10-127-835A-446	Sequence 446, App
402	23	100.0	180	10	US-09-816-744-2	Sequence 2, Appli	475	23	100.0	180	14	US-10-127-839A-446	Sequence 446, App
403	23	100.0	180	10	US-09-978-189-470	Sequence 470, App	476	23	100.0	180	14	US-10-127-901A-446	Sequence 446, App
404	23	100.0	180	10	US-09-747-259-2	Sequence 2, Appli	477	23	100.0	180	14	US-10-128-693A-446	Sequence 446, App
405	23	100.0	180	10	US-09-978-608A-470	Sequence 470, App	478	23	100.0	180	14	US-10-131-813A-446	Sequence 446, App
406	23	100.0	180	10	US-09-978-585A-470	Sequence 470, App	479	23	100.0	180	14	US-10-131-818A-446	Sequence 446, App
407	23	100.0	180	10	US-09-978-191A-470	Sequence 470, App	480	23	100.0	180	14	US-10-131-823A-446	Sequence 446, App
408	23	100.0	180	10	US-09-978-403A-470	Sequence 470, App	481	23	100.0	180	14	US-10-131-824A-446	Sequence 446, App
409	23	100.0	180	10	US-09-978-564A-470	Sequence 470, App	482	23	100.0	180	14	US-10-131-830A-446	Sequence 446, App
410	23	100.0	180	10	US-09-999-833A-470	Sequence 470, App	483	23	100.0	180	14	US-10-131-837A-446	Sequence 446, App
411	23	100.0	180	10	US-09-908-827-2	Sequence 2, Appli	484	23	100.0	180	14	US-10-137-872A-446	Sequence 446, App
412	23	100.0	180	10	US-09-981-915A-470	Sequence 470, App	485	23	100.0	180	14	US-10-147-500-446	Sequence 446, App
413	23	100.0	180	10	US-09-978-824-470	Sequence 470, App	486	23	100.0	180	14	US-10-147-502-446	Sequence 446, App
414	23	100.0	180	10	US-09-918-585A-470	Sequence 470, App	487	23	100.0	180	14	US-10-147-515-446	Sequence 446, App
415	23	100.0	180	10	US-09-999-834A-470	Sequence 470, App	488	23	100.0	180	14	US-10-147-517-446	Sequence 446, App
416	23	100.0	180	10	US-09-978-423A-470	Sequence 470, App	489	23	100.0	180	14	US-10-147-526-446	Sequence 446, App
417	23	100.0	180	10	US-09-978-193A-470	Sequence 470, App	490	23	100.0	180	14	US-10-147-537-446	Sequence 446, App
418	23	100.0	180	10	US-09-999-830A-470	Sequence 470, App	491	23	100.0	180	14	US-10-121-041-446	Sequence 446, App
419	23	100.0	180	10	US-09-774-381-2	Sequence 2, Appli	492	23	100.0	180	14	US-10-121-043-446	Sequence 446, App
420	23	100.0	180	10	US-09-978-757A-470	Sequence 470, App	493	23	100.0	180	14	US-10-121-047-446	Sequence 446, App
421	23	100.0	180	10	US-09-978-187B-470	Sequence 470, App	494	23	100.0	180	14	US-10-123-215-446	Sequence 446, App
422	23	100.0	180	10	US-09-978-643A-470	Sequence 470, App	495	23	100.0	180	14	US-10-123-902-446	Sequence 446, App
423	23	100.0	180	10	US-09-978-375A-470	Sequence 470, App	496	23	100.0	180	14	US-10-123-908-446	Sequence 446, App
424	23	100.0	180	10	US-09-978-298A-470	Sequence 470, App	497	23	100.0	180	14	US-10-123-909-446	Sequence 446, App
425	23	100.0	180	10	US-09-978-188A-470	Sequence 470, App	498	23	100.0	180	14	US-10-123-910-446	Sequence 446, App
426	23	100.0	180	10	US-09-978-665A-470	Sequence 470, App	499	23	100.0	180	14	US-10-124-813-446	Sequence 446, App
427	23	100.0	180	10	US-09-978-194A-470	Sequence 470, App	500	23	100.0	180	14	US-10-124-817-446	Sequence 446, App
428	23	100.0	180	10	US-09-999-829A-470	Sequence 470, App	501	23	100.0	180	14	US-10-125-922-446	Sequence 446, App
429	23	100.0	180	10	US-09-978-299A-470	Sequence 470, App	502	23	100.0	180	14	US-10-125-924-446	Sequence 446, App
430	23	100.0	180	10	US-09-978-544A-470	Sequence 470, App	503	23	100.0	180	14	US-10-140-860-446	Sequence 446, App
431	23	100.0	180	10	US-09-978-65A-470	Sequence 470, App	504	23	100.0	180	14	US-10-142-817-446	Sequence 446, App
432	23	100.0	180	10	US-09-978-802A-470	Sequence 470, App	505	23	100.0	180	14	US-10-147-519-446	Sequence 446, App
433	23	100.0	180	11	US-09-999-831A-470	Sequence 35, Appl	506	23	100.0	180	14	US-10-157-782-446	Sequence 446, App
434	23	100.0	180	11	US-09-796-844-35	Sequence 35, Appl	507	23	100.0	180	14	US-10-152-395-446	Sequence 446, App
435	23	100.0	180	13	US-10-000-157-2	Sequence 2, Appli	508	23	100.0	180	14	US-10-125-926A-446	Sequence 446, App
436	23	100.0	180	14	US-10-028-072-446	Sequence 446, App	509	23	100.0	180	14	US-10-125-930A-446	Sequence 446, App
437	23	100.0	180	14	US-10-140-808-446	Sequence 446, App	510	23	100.0	180	14	US-10-127-831A-446	Sequence 446, App
438	23	100.0	180	14	US-10-121-049-446	Sequence 446, App	511	23	100.0	180	14	US-10-127-837A-446	Sequence 446, App
439	23	100.0	180	14	US-10-123-904-446	Sequence 446, App	512	23	100.0	180	14	US-10-127-838B-446	Sequence 446, App
440	23	100.0	180	14	US-10-140-470-446	Sequence 446, App	513	23	100.0	180	14	US-10-127-842A-446	Sequence 446, App
441	23	100.0	180	14	US-10-175-746-446	Sequence 446, App	514	23	100.0	180	14	US-10-127-843A-446	Sequence 446, App
442	23	100.0	180	14	US-10-176-918-446	Sequence 446, App	515	23	100.0	180	14	US-10-127-845A-446	Sequence 446, App
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444	23	100.0	180	14	US-10-137-865-446	Sequence 446, App	517	23	100.0	180	14	US-10-127-848A-446	Sequence 446, App
445	23	100.0	180	14	US-10-140-474-446	Sequence 446, App	518	23	100.0	180	14	US-10-127-849A-446	Sequence 446, App
446	23	100.0	180	14	US-10-142-431-446	Sequence 446, App	519	23	100.0	180	14	US-10-127-850A-446	Sequence 446, App
447	23	100.0	180	14	US-10-143-114-446	Sequence 446, App	520	23	100.0	180	14	US-10-127-851A-446	Sequence 446, App
448	23	100.0	180	14	US-10-142-419-446	Sequence 446, App	521	23	100.0	180	14	US-10-128-684A-446	Sequence 446, App
449	23	100.0	180	14	US-10-017-081A-470	Sequence 470, App	522	23	100.0	180	14	US-10-128-686A-446	Sequence 446, App
450	23	100.0	180	14	US-10-123-262-446	Sequence 446, App	523	23	100.0	180	14	US-10-128-690A-446	Sequence 446, App
451	23	100.0	180	14	US-10-142-423-446	Sequence 446, App	524	23	100.0	180	14	US-10-128-691A-446	Sequence 446, App

525	23	100.0	180	14	US-10-131-819A-446	Sequence 446, App	598	23	100.0	180	14	US-10-142-421-446	Sequence 446, App
526	23	100.0	180	14	US-10-131-829A-446	Sequence 446, App	599	23	100.0	180	14	US-10-142-432-446	Sequence 446, App
527	23	100.0	180	14	US-10-131-836A-446	Sequence 446, App	600	23	100.0	180	14	US-10-142-767-446	Sequence 446, App
528	23	100.0	180	14	US-10-146-729-446	Sequence 446, App	601	23	100.0	180	14	US-10-143-033-446	Sequence 446, App
529	23	100.0	180	14	US-10-146-791-446	Sequence 446, App	602	23	100.0	180	14	US-10-144-994-446	Sequence 446, App
530	23	100.0	180	14	US-10-147-484-446	Sequence 446, App	603	23	100.0	180	14	US-10-145-628-446	Sequence 446, App
531	23	100.0	180	14	US-10-147-508-446	Sequence 446, App	604	23	100.0	180	14	US-10-145-628-446	Sequence 446, App
532	23	100.0	180	14	US-10-147-512-446	Sequence 446, App	605	23	100.0	180	14	US-10-145-746-446	Sequence 446, App
533	23	100.0	180	14	US-10-175-735-446	Sequence 446, App	606	23	100.0	180	14	US-10-145-748-446	Sequence 446, App
534	23	100.0	180	14	US-10-121-040-446	Sequence 446, App	607	23	100.0	180	14	US-10-145-823-446	Sequence 446, App
535	23	100.0	180	14	US-10-121-056-446	Sequence 446, App	608	23	100.0	180	14	US-10-145-826-446	Sequence 446, App
536	23	100.0	180	14	US-10-121-061-446	Sequence 446, App	609	23	100.0	180	14	US-10-145-870-446	Sequence 446, App
537	23	100.0	180	14	US-10-123-235-446	Sequence 446, App	610	23	100.0	180	14	US-10-145-876-446	Sequence 446, App
538	23	100.0	180	14	US-10-124-818-446	Sequence 446, App	611	23	100.0	180	14	US-10-145-959-446	Sequence 446, App
539	23	100.0	180	14	US-10-137-868-446	Sequence 446, App	612	23	100.0	180	14	US-10-146-724-446	Sequence 446, App
540	23	100.0	180	14	US-10-147-492-446	Sequence 446, App	613	23	100.0	180	14	US-10-146-725-446	Sequence 446, App
541	23	100.0	180	14	US-10-158-782-446	Sequence 446, App	614	23	100.0	180	14	US-10-146-795-446	Sequence 446, App
542	23	100.0	180	14	US-10-123-905-446	Sequence 446, App	615	23	100.0	180	14	US-10-147-495-446	Sequence 446, App
543	23	100.0	180	14	US-10-123-907-446	Sequence 446, App	616	23	100.0	180	14	US-10-147-501-446	Sequence 446, App
544	23	100.0	180	14	US-10-124-815-446	Sequence 446, App	617	23	100.0	180	14	US-10-147-504-446	Sequence 446, App
545	23	100.0	180	14	US-10-125-921A-446	Sequence 446, App	618	23	100.0	180	14	US-10-147-506-446	Sequence 446, App
546	23	100.0	180	14	US-10-125-928A-446	Sequence 446, App	619	23	100.0	180	14	US-10-147-509-446	Sequence 446, App
547	23	100.0	180	14	US-10-127-821A-446	Sequence 446, App	620	23	100.0	180	14	US-10-147-510-446	Sequence 446, App
548	23	100.0	180	14	US-10-127-822A-446	Sequence 446, App	621	23	100.0	180	14	US-10-147-511-446	Sequence 446, App
549	23	100.0	180	14	US-10-127-824A-446	Sequence 446, App	622	23	100.0	180	14	US-10-147-529-446	Sequence 446, App
550	23	100.0	180	14	US-10-127-826A-446	Sequence 446, App	623	23	100.0	180	14	US-10-152-397-446	Sequence 446, App
551	23	100.0	180	14	US-10-127-827A-446	Sequence 446, App	624	23	100.0	180	14	US-10-153-585-446	Sequence 446, App
552	23	100.0	180	14	US-10-127-828A-446	Sequence 446, App	625	23	100.0	180	14	US-10-158-786-446	Sequence 446, App
553	23	100.0	180	14	US-10-127-830A-446	Sequence 446, App	626	23	100.0	180	14	US-10-143-031A-470	Sequence 470, App
554	23	100.0	180	14	US-10-127-832A-446	Sequence 446, App	627	23	100.0	180	14	US-10-137-870-446	Sequence 446, App
555	23	100.0	180	14	US-10-127-833A-446	Sequence 446, App	628	23	100.0	180	14	US-10-140-018-446	Sequence 446, App
556	23	100.0	180	14	US-10-127-834A-446	Sequence 446, App	629	23	100.0	180	14	US-10-140-021-446	Sequence 446, App
557	23	100.0	180	14	US-10-127-836A-446	Sequence 446, App	630	23	100.0	180	14	US-10-140-471-446	Sequence 446, App
558	23	100.0	180	14	US-10-127-841A-446	Sequence 446, App	631	23	100.0	180	14	US-10-140-922-446	Sequence 446, App
559	23	100.0	180	14	US-10-127-844A-446	Sequence 446, App	632	23	100.0	180	14	US-10-145-631-446	Sequence 446, App
560	23	100.0	180	14	US-10-128-687A-446	Sequence 446, App	633	23	100.0	180	14	US-10-145-633-446	Sequence 446, App
561	23	100.0	180	14	US-10-128-688A-446	Sequence 446, App	634	23	100.0	180	14	US-10-158-783-446	Sequence 446, App
562	23	100.0	180	14	US-10-128-689A-446	Sequence 446, App	635	23	100.0	180	14	US-10-340-042-2	Sequence 2, Appli
563	23	100.0	180	14	US-10-128-694A-446	Sequence 446, App	636	23	100.0	180	14	US-10-140-274-446	Sequence 446, App
564	23	100.0	180	14	US-10-131-825A-446	Sequence 446, App	637	23	100.0	180	14	US-10-143-030A-470	Sequence 470, App
565	23	100.0	180	14	US-10-230-417-446	Sequence 446, App	638	23	100.0	180	14	US-10-002-967A-470	Sequence 470, App
566	23	100.0	180	14	US-10-131-815A-446	Sequence 446, App	639	23	100.0	180	14	US-10-017-083A-470	Sequence 470, App
567	23	100.0	180	14	US-10-131-817A-446	Sequence 446, App	640	23	100.0	180	14	US-10-140-019-446	Sequence 446, App
568	23	100.0	180	14	US-10-131-821A-446	Sequence 446, App	641	23	100.0	180	14	US-10-140-032-446	Sequence 446, App
569	23	100.0	180	14	US-10-131-822A-446	Sequence 446, App	642	23	100.0	180	14	US-10-140-861-446	Sequence 446, App
570	23	100.0	180	14	US-10-131-828A-446	Sequence 446, App	643	23	100.0	180	14	US-10-140-862-446	Sequence 446, App
571	23	100.0	180	14	US-10-131-835A-446	Sequence 446, App	644	23	100.0	180	14	US-10-141-697-446	Sequence 446, App
572	23	100.0	180	14	US-10-137-864A-446	Sequence 446, App	645	23	100.0	180	14	US-10-141-700-446	Sequence 446, App
573	23	100.0	180	14	US-10-137-869A-446	Sequence 446, App	646	23	100.0	180	14	US-10-141-705-446	Sequence 446, App
574	23	100.0	180	14	US-10-147-523-446	Sequence 446, App	647	23	100.0	180	14	US-10-141-753-446	Sequence 446, App
575	23	100.0	180	14	US-10-158-785-446	Sequence 446, App	648	23	100.0	180	14	US-10-142-418-446	Sequence 446, App
576	23	100.0	180	14	US-10-153-770-8	Sequence 8, Appli	649	23	100.0	180	14	US-10-142-420-446	Sequence 446, App
577	23	100.0	180	14	US-10-121-051-446	Sequence 446, App	650	23	100.0	180	14	US-10-142-422-446	Sequence 446, App
578	23	100.0	180	14	US-10-121-042-446	Sequence 446, App	651	23	100.0	180	14	US-10-142-427-446	Sequence 446, App
579	23	100.0	180	14	US-10-123-912-446	Sequence 446, App	652	23	100.0	180	14	US-10-142-760-446	Sequence 446, App
580	23	100.0	180	14	US-10-166-709A-470	Sequence 470, App	653	23	100.0	180	14	US-10-145-821-446	Sequence 446, App
581	23	100.0	180	14	US-10-192-007-446	Sequence 446, App	654	23	100.0	180	14	US-10-152-531-446	Sequence 446, App
582	23	100.0	180	14	US-10-194-359-446	Sequence 446, App	655	23	100.0	180	14	US-10-127-840A-446	Sequence 446, App
583	23	100.0	180	14	US-10-253-159-2	Sequence 2, Appli	656	23	100.0	180	14	US-10-142-424-446	Sequence 446, App
584	23	100.0	180	14	US-10-156-761-11409	Sequence 11409, A	657	23	100.0	180	14	US-10-142-761-446	Sequence 446, App
585	23	100.0	180	14	US-10-127-847A-446	Sequence 446, App	658	23	100.0	180	14	US-10-142-763-446	Sequence 446, App
586	23	100.0	180	14	US-10-137-866-446	Sequence 446, App	659	23	100.0	180	14	US-10-142-765-446	Sequence 446, App
587	23	100.0	180	14	US-10-146-726-446	Sequence 446, App	660	23	100.0	180	14	US-10-142-887-446	Sequence 446, App
588	23	100.0	180	14	US-10-146-727-446	Sequence 446, App	661	23	100.0	180	14	US-10-142-888-446	Sequence 446, App
589	23	100.0	180	14	US-10-146-788-446	Sequence 446, App	662	23	100.0	180	14	US-10-143-034-446	Sequence 446, App
590	23	100.0	180	14	US-10-152-380-446	Sequence 446, App	663	23	100.0	180	14	US-10-143-116-446	Sequence 446, App
591	23	100.0	180	14	US-10-153-934-446	Sequence 446, App	664	23	100.0	180	14	US-10-144-957-446	Sequence 446, App
592	23	100.0	180	14	US-10-140-807-446	Sequence 446, App	665	23	100.0	180	14	US-10-144-992-446	Sequence 446, App
593	23	100.0	180	14	US-10-140-924-446	Sequence 446, App	666	23	100.0	180	14	US-10-145-015-446	Sequence 446, App
594	23	100.0	180	14	US-10-140-926-446	Sequence 446, App	667	23	100.0	180	14	US-10-145-090-446	Sequence 446, App
595	23	100.0	180	14	US-10-141-698-446	Sequence 446, App	668	23	100.0	180	14	US-10-145-091-446	Sequence 446, App
596	23	100.0	180	14	US-10-141-702-446	Sequence 446, App	669	23	100.0	180	14	US-10-145-128A-470	Sequence 470, App
597	23	100.0	180	14	US-10-141-704-446	Sequence 446, App	670	23	100.0	180	14	US-10-145-629-446	Sequence 446, App

671	23	100.0	180	14	US-10-145-630-446	Sequence 446, App	744	23	100.0	180	14	US-10-145-960-446	Sequence 446, App
672	23	100.0	180	14	US-10-145-747-446	Sequence 446, App	745	23	100.0	180	14	US-10-145-962-446	Sequence 446, App
673	23	100.0	180	14	US-10-145-752-446	Sequence 446, App	746	23	100.0	180	14	US-10-146-789-446	Sequence 446, App
674	23	100.0	180	14	US-10-145-754-446	Sequence 446, App	747	23	100.0	180	14	US-10-147-483-446	Sequence 446, App
675	23	100.0	180	14	US-10-145-755-446	Sequence 446, App	748	23	100.0	180	14	US-10-147-496-446	Sequence 446, App
676	23	100.0	180	14	US-10-145-818-446	Sequence 446, App	749	23	100.0	180	14	US-10-147-505-446	Sequence 446, App
677	23	100.0	180	14	US-10-145-822-446	Sequence 446, App	750	23	100.0	180	14	US-10-147-516-446	Sequence 446, App
678	23	100.0	180	14	US-10-145-872-446	Sequence 446, App	751	23	100.0	180	14	US-10-152-398-446	Sequence 446, App
679	23	100.0	180	14	US-10-145-873-446	Sequence 446, App	752	23	100.0	180	14	US-10-152-398-446	Sequence 446, App
680	23	100.0	180	14	US-10-147-481-446	Sequence 446, App	753	23	100.0	180	14	US-10-277-726A-2	Sequence 2, Appli
681	23	100.0	180	14	US-10-147-482-446	Sequence 446, App	754	23	100.0	180	14	US-10-139-980-446	Sequence 446, App
682	23	100.0	180	14	US-10-147-503-446	Sequence 446, App	755	23	100.0	180	14	US-10-165-067A-470	Sequence 470, App
683	23	100.0	180	14	US-10-147-522-446	Sequence 446, App	756	23	100.0	180	14	US-10-410-374-2	Sequence 2, Appli
684	23	100.0	180	14	US-10-152-401-446	Sequence 446, App	757	23	100.0	180	14	US-10-145-017A-470	Sequence 470, App
685	23	100.0	180	14	US-10-157-783-446	Sequence 446, App	758	23	100.0	180	14	US-10-145-750-446	Sequence 446, App
686	23	100.0	180	14	US-10-158-792-446	Sequence 446, App	759	23	100.0	180	14	US-10-152-373-446	Sequence 446, App
687	23	100.0	180	14	US-10-158-462-446	Sequence 446, App	760	23	100.0	180	14	US-10-164-728A-470	Sequence 470, App
688	23	100.0	180	14	US-10-143-035-446	Sequence 446, App	761	23	100.0	180	14	US-10-397-282-8	Sequence 8, Appli
689	23	100.0	180	14	US-10-145-751-446	Sequence 446, App	762	23	100.0	180	14	US-10-013-926A-470	Sequence 470, App
690	23	100.0	180	14	US-10-145-822-446	Sequence 446, App	763	23	100.0	180	14	US-10-165-247A-470	Sequence 470, App
691	23	100.0	180	14	US-10-145-824-446	Sequence 446, App	764	23	100.0	180	14	US-10-145-124A-470	Sequence 470, App
692	23	100.0	180	14	US-10-145-827-446	Sequence 446, App	765	23	100.0	180	14	US-10-160-502A-470	Sequence 470, App
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694	23	100.0	180	14	US-10-145-875-446	Sequence 446, App	767	23	100.0	180	14	US-10-121-055-446	Sequence 446, App
695	23	100.0	180	14	US-10-145-877-446	Sequence 446, App	768	23	100.0	180	14	US-10-121-057-446	Sequence 446, App
696	23	100.0	180	14	US-10-145-958-446	Sequence 446, App	769	23	100.0	180	14	US-10-121-058-446	Sequence 446, App
697	23	100.0	180	14	US-10-146-787-446	Sequence 446, App	770	23	100.0	180	14	US-10-121-059-446	Sequence 446, App
698	23	100.0	180	14	US-10-146-790-446	Sequence 446, App	771	23	100.0	180	14	US-10-121-060-446	Sequence 446, App
699	23	100.0	180	14	US-10-146-793-446	Sequence 446, App	772	23	100.0	180	14	US-10-123-109-446	Sequence 446, App
700	23	100.0	180	14	US-10-147-480-446	Sequence 446, App	773	23	100.0	180	14	US-10-123-154-446	Sequence 446, App
701	23	100.0	180	14	US-10-147-485-446	Sequence 446, App	774	23	100.0	180	14	US-10-123-157-446	Sequence 446, App
702	23	100.0	180	14	US-10-147-486-446	Sequence 446, App	775	23	100.0	180	14	US-10-123-906-446	Sequence 446, App
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704	23	100.0	180	14	US-10-147-490-446	Sequence 446, App	777	23	100.0	180	14	US-10-124-816-446	Sequence 446, App
705	23	100.0	180	14	US-10-147-494-446	Sequence 446, App	778	23	100.0	180	14	US-10-124-820-446	Sequence 446, App
706	23	100.0	180	14	US-10-147-498-446	Sequence 446, App	779	23	100.0	180	14	US-10-125-704-446	Sequence 446, App
707	23	100.0	180	14	US-10-147-514-446	Sequence 446, App	780	23	100.0	180	14	US-10-125-927-446	Sequence 446, App
708	23	100.0	180	14	US-10-147-524-446	Sequence 446, App	781	23	100.0	180	14	US-10-145-087A-470	Sequence 470, App
709	23	100.0	180	14	US-10-152-379-446	Sequence 446, App	782	23	100.0	180	14	US-10-017-889A-470	Sequence 470, App
710	23	100.0	180	14	US-10-152-394-446	Sequence 446, App	783	23	100.0	180	14	US-10-142-889-446	Sequence 446, App
711	23	100.0	180	14	US-10-152-406-446	Sequence 446, App	784	23	100.0	180	14	US-10-145-874-446	Sequence 446, App
712	23	100.0	180	14	US-10-156-847-446	Sequence 446, App	785	23	100.0	180	14	US-10-147-497-446	Sequence 446, App
713	23	100.0	180	14	US-10-157-778-446	Sequence 446, App	786	23	100.0	180	14	US-10-152-371-446	Sequence 446, App
714	23	100.0	180	14	US-10-157-799-446	Sequence 446, App	787	23	100.0	180	14	US-10-152-374-446	Sequence 446, App
715	23	100.0	180	14	US-10-160-504-446	Sequence 446, App	788	23	100.0	180	14	US-10-152-375-446	Sequence 446, App
716	23	100.0	180	14	US-10-017-191A-470	Sequence 470, App	789	23	100.0	180	14	US-10-152-377-446	Sequence 446, App
717	23	100.0	180	14	US-10-145-634-446	Sequence 446, App	790	23	100.0	180	14	US-10-152-386-446	Sequence 446, App
718	23	100.0	180	14	US-10-147-520-446	Sequence 446, App	791	23	100.0	180	14	US-10-152-391-446	Sequence 446, App
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722	23	100.0	180	14	US-10-147-491-446	Sequence 446, App	795	23	100.0	180	14	US-10-157-794-446	Sequence 446, App
723	23	100.0	180	14	US-10-152-378-446	Sequence 446, App	796	23	100.0	180	14	US-10-157-796-446	Sequence 446, App
724	23	100.0	180	14	US-10-152-382-446	Sequence 446, App	797	23	100.0	180	14	US-10-157-796-446	Sequence 446, App
725	23	100.0	180	14	US-10-152-383-446	Sequence 446, App	798	23	100.0	180	14	US-10-160-500-446	Sequence 446, App
726	23	100.0	180	14	US-10-152-384-446	Sequence 446, App	799	23	100.0	180	14	US-10-164-829A-470	Sequence 470, App
727	23	100.0	180	14	US-10-152-387-446	Sequence 446, App	800	23	100.0	180	14	US-10-164-929A-470	Sequence 470, App
728	23	100.0	180	14	US-10-152-389-446	Sequence 446, App	801	23	100.0	180	14	US-10-121-046-446	Sequence 446, App
729	23	100.0	180	14	US-10-152-390-446	Sequence 446, App	802	23	100.0	180	14	US-10-123-156-446	Sequence 446, App
730	23	100.0	180	14	US-10-152-392-446	Sequence 446, App	803	23	100.0	180	14	US-10-123-214-446	Sequence 446, App
731	23	100.0	180	14	US-10-153-756-446	Sequence 446, App	804	23	100.0	180	14	US-10-125-805-446	Sequence 446, App
732	23	100.0	180	14	US-10-157-784-446	Sequence 446, App	805	23	100.0	180	14	US-10-013-922A-470	Sequence 470, App
733	23	100.0	180	14	US-10-157-797-446	Sequence 446, App	806	23	100.0	180	14	US-10-020-445A-470	Sequence 470, App
734	23	100.0	180	14	US-10-158-491-446	Sequence 446, App	807	23	100.0	180	14	US-10-013-924A-470	Sequence 470, App
735	23	100.0	180	14	US-10-410-927-2	Sequence 2, Appli	808	23	100.0	180	14	US-10-124-821-446	Sequence 446, App
736	23	100.0	180	14	US-10-143-028A-470	Sequence 470, App	809	23	100.0	180	14	US-10-152-385-446	Sequence 446, App
737	23	100.0	180	14	US-10-143-029A-470	Sequence 470, App	810	23	100.0	180	14	US-10-152-396-446	Sequence 446, App
738	23	100.0	180	14	US-10-142-762-446	Sequence 446, App	811	23	100.0	180	14	US-10-153-552-446	Sequence 446, App
739	23	100.0	180	14	US-10-142-764-446	Sequence 446, App	812	23	100.0	180	14	US-10-153-840-446	Sequence 446, App
740	23	100.0	180	14	US-10-142-766-446	Sequence 446, App	813	23	100.0	180	14	US-10-156-841-446	Sequence 446, App
741	23	100.0	180	14	US-10-145-089A-470	Sequence 470, App	814	23	100.0	180	14	US-10-156-842-446	Sequence 446, App
742	23	100.0	180	14	US-10-145-625-446	Sequence 446, App	815	23	100.0	180	14	US-10-156-844-446	Sequence 446, App
743	23	100.0	180	14	US-10-145-627-446	Sequence 446, App	816	23	100.0	180	14	US-10-156-845-446	Sequence 446, App
												US-10-156-846-446	Sequence 446, App

817	23	100.0	180	14	US-10-410-552-2	Sequence 2, Appli	890	23	100.0	180	15	US-10-158-784-446	Sequence 446, App
818	23	100.0	180	14	US-10-121-048-446	Sequence 446, App	891	23	100.0	180	15	US-10-158-789-446	Sequence 446, App
819	23	100.0	180	14	US-10-121-052-446	Sequence 446, App	892	23	100.0	180	15	US-10-192-011-446	Sequence 446, App
820	23	100.0	180	14	US-10-121-053-446	Sequence 446, App	893	23	100.0	180	15	US-10-139-963-446	Sequence 446, App
821	23	100.0	180	14	US-10-121-054-446	Sequence 446, App	894	23	100.0	180	15	US-10-140-020-446	Sequence 446, App
822	23	100.0	180	14	US-10-121-063-446	Sequence 446, App	895	23	100.0	180	15	US-10-140-023-446	Sequence 446, App
823	23	100.0	180	14	US-10-123-212-446	Sequence 446, App	896	23	100.0	180	15	US-10-140-809-446	Sequence 446, App
824	23	100.0	180	14	US-10-123-213-446	Sequence 446, App	897	23	100.0	180	15	US-10-140-809-446	Sequence 446, App
825	23	100.0	180	14	US-10-123-291-446	Sequence 446, App	898	23	100.0	180	15	US-10-140-865-446	Sequence 446, App
826	23	100.0	180	14	US-10-123-322-446	Sequence 446, App	899	23	100.0	180	15	US-10-141-701-446	Sequence 446, App
827	23	100.0	180	14	US-10-123-771-446	Sequence 446, App	900	23	100.0	180	15	US-10-141-754-446	Sequence 446, App
828	23	100.0	180	14	US-10-123-911-446	Sequence 446, App	901	23	100.0	180	15	US-10-141-760-446	Sequence 446, App
829	23	100.0	180	14	US-10-124-823-446	Sequence 446, App	902	23	100.0	180	15	US-10-142-430-446	Sequence 446, App
830	23	100.0	180	14	US-10-125-931-446	Sequence 446, App	903	23	100.0	180	15	US-10-143-113-446	Sequence 446, App
831	23	100.0	180	14	US-10-125-932-446	Sequence 446, App	904	23	100.0	180	15	US-10-146-730-446	Sequence 446, App
832	23	100.0	180	15	US-10-125-932-446	Sequence 446, App	905	23	100.0	180	15	US-10-146-732-446	Sequence 446, App
833	23	100.0	180	15	US-10-127-852A-446	Sequence 446, App	906	23	100.0	180	15	US-10-158-731-446	Sequence 446, App
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835	23	100.0	180	15	US-10-128-685A-446	Sequence 446, App	908	23	100.0	180	15	US-10-158-731-446	Sequence 446, App
836	23	100.0	180	15	US-10-131-820A-446	Sequence 446, App	909	23	100.0	180	15	US-10-158-731-446	Sequence 446, App
837	23	100.0	180	15	US-10-143-886-446	Sequence 446, App	910	23	100.0	180	15	US-10-157-786-446	Sequence 446, App
838	23	100.0	180	15	US-10-145-016A-470	Sequence 446, App	911	23	100.0	180	15	US-10-013-918A-470	Sequence 446, App
839	23	100.0	180	15	US-10-145-088A-470	Sequence 446, App	912	23	100.0	180	15	US-10-162-521A-470	Sequence 446, App
840	23	100.0	180	15	US-10-145-088A-470	Sequence 446, App	913	23	100.0	180	15	US-10-152-405-446	Sequence 446, App
841	23	100.0	180	15	US-10-145-129A-470	Sequence 446, App	914	23	100.0	180	15	US-10-013-928A-470	Sequence 446, App
842	23	100.0	180	15	US-10-146-728-446	Sequence 446, App	915	23	100.0	180	15	US-10-162-522A-470	Sequence 446, App
843	23	100.0	180	15	US-10-146-786-446	Sequence 446, App	916	23	100.0	180	15	US-10-013-923A-470	Sequence 446, App
844	23	100.0	180	15	US-10-147-499-446	Sequence 446, App	917	23	100.0	180	15	US-10-013-925A-470	Sequence 446, App
845	23	100.0	180	15	US-10-157-798-446	Sequence 446, App	918	23	100.0	180	15	US-10-013-927A-470	Sequence 446, App
846	23	100.0	180	15	US-10-165-038A-470	Sequence 446, App	919	23	100.0	180	15	US-10-147-528-446	Sequence 446, App
847	23	100.0	180	15	US-10-165-353A-470	Sequence 446, App	920	23	100.0	180	15	US-10-145-093A-470	Sequence 446, App
848	23	100.0	180	15	US-10-167-600-470	Sequence 446, App	921	23	100.0	180	15	US-10-013-919A-470	Sequence 446, App
849	23	100.0	180	15	US-10-170-481A-470	Sequence 446, App	922	23	100.0	180	15	US-10-013-920A-470	Sequence 446, App
850	23	100.0	180	15	US-10-172-039A-470	Sequence 446, App	923	23	100.0	180	15	US-10-128-692A-446	Sequence 446, App
851	23	100.0	180	15	US-10-210-028-470	Sequence 446, App	924	23	100.0	180	15	US-10-140-927-446	Sequence 446, App
852	23	100.0	180	15	US-10-458-442-2	Sequence 2, Appli	925	23	100.0	180	15	US-10-147-493-446	Sequence 446, App
853	23	100.0	180	15	US-10-123-913-446	Sequence 446, App	926	23	100.0	180	15	US-10-145-127-446	Sequence 446, App
854	23	100.0	180	15	US-10-017-085A-470	Sequence 446, App	927	23	100.0	180	15	US-10-145-127-446	Sequence 446, App
855	23	100.0	180	15	US-10-013-916A-470	Sequence 446, App	928	23	100.0	180	15	US-10-160-503-446	Sequence 446, App
856	23	100.0	180	15	US-10-140-473-446	Sequence 446, App	929	23	100.0	180	15	US-10-143-118-446	Sequence 446, App
857	23	100.0	180	15	US-10-140-806-446	Sequence 446, App	930	23	100.0	180	15	US-10-144-933-446	Sequence 446, App
858	23	100.0	180	15	US-10-140-810-446	Sequence 446, App	931	23	100.0	180	15	US-10-158-787-446	Sequence 446, App
859	23	100.0	180	15	US-10-140-863-446	Sequence 446, App	932	23	100.0	180	15	US-10-408-385-2	Sequence 2, Appli
860	23	100.0	180	15	US-10-141-699-446	Sequence 446, App	933	23	100.0	180	15	US-10-140-024-446	Sequence 446, App
861	23	100.0	180	15	US-10-141-703-446	Sequence 446, App	934	23	100.0	180	15	US-10-013-917A-470	Sequence 446, App
862	23	100.0	180	15	US-10-141-705-446	Sequence 446, App	935	23	100.0	180	15	US-10-147-536-446	Sequence 446, App
863	23	100.0	180	15	US-10-141-757-446	Sequence 446, App	936	23	100.0	180	16	US-10-645-702-35	Sequence 35, Appli
864	23	100.0	180	15	US-10-142-428-446	Sequence 446, App	937	23	100.0	180	16	US-10-742-220-2	Sequence 2, Appli
865	23	100.0	180	15	US-10-142-428-446	Sequence 446, App	938	23	100.0	180	16	US-10-437-963-135103	Sequence 135103,
866	23	100.0	180	15	US-10-142-429-446	Sequence 446, App	939	23	100.0	180	16	US-10-152-372-446	Sequence 446, App
867	23	100.0	180	15	US-10-142-884-446	Sequence 446, App	940	23	100.0	180	16	US-10-772-985-2	Sequence 2, Appli
868	23	100.0	180	15	US-10-143-027-446	Sequence 446, App	941	23	100.0	180	16	US-10-416-424-51	Sequence 51, Appli
869	23	100.0	180	15	US-10-143-115-446	Sequence 446, App	942	23	100.0	180	17	US-10-918-851-470	Sequence 470, App
870	23	100.0	180	15	US-10-144-956-446	Sequence 446, App	943	23	100.0	180	17	US-10-931-886-446	Sequence 446, App
871	23	100.0	180	15	US-10-144-958-446	Sequence 446, App	944	23	100.0	180	17	US-10-805-667-470	Sequence 470, App
872	23	100.0	180	15	US-10-145-632-446	Sequence 446, App	945	23	100.0	180	17	US-10-897-359-470	Sequence 470, App
873	23	100.0	180	15	US-10-145-749-446	Sequence 446, App	946	23	100.0	180	17	US-10-158-788-446	Sequence 446, App
874	23	100.0	180	15	US-10-145-753-446	Sequence 446, App	947	23	100.0	180	17	US-10-893-802-470	Sequence 470, App
875	23	100.0	180	15	US-10-145-871-446	Sequence 446, App	948	23	100.0	180	17	US-10-897-360-470	Sequence 470, App
876	23	100.0	180	15	US-10-145-878-446	Sequence 446, App	949	23	100.0	181	15	US-10-425-114-49549	Sequence 49549, A
877	23	100.0	180	15	US-10-146-794-446	Sequence 446, App	950	23	100.0	181	15	US-10-425-114-66671	Sequence 66671, A
878	23	100.0	180	15	US-10-147-489-446	Sequence 446, App	951	23	100.0	182	16	US-10-437-963-109627	Sequence 109627,
879	23	100.0	180	15	US-10-147-507-446	Sequence 446, App	952	23	100.0	183	15	US-10-424-599-194937	Sequence 194937,
880	23	100.0	180	15	US-10-147-535-446	Sequence 446, App	953	23	100.0	183	15	US-10-425-114-49344	Sequence 49344, A
881	23	100.0	180	15	US-10-147-537-446	Sequence 446, App	954	23	100.0	184	14	US-10-106-698-5135	Sequence 5135, Ap
882	23	100.0	180	15	US-10-152-376-446	Sequence 446, App	955	23	100.0	184	16	US-10-424-599-208647	Sequence 208647,
883	23	100.0	180	15	US-10-152-381-446	Sequence 446, App	956	23	100.0	184	16	US-10-437-963-188586	Sequence 188586,
884	23	100.0	180	15	US-10-152-400-446	Sequence 446, App	957	23	100.0	185	15	US-10-369-493-6227	Sequence 6227, Ap
885	23	100.0	180	15	US-10-153-585-446	Sequence 446, App	958	23	100.0	185	16	US-10-363-829-265	Sequence 265, App
886	23	100.0	180	15	US-10-157-800-446	Sequence 446, App	959	23	100.0	186	15	US-10-074-024-321	Sequence 321, App
887	23	100.0	180	15	US-10-157-800-446	Sequence 446, App	960	23	100.0	186	15	US-10-424-599-209344	Sequence 209344,
888	23	100.0	180	15	US-10-157-801-446	Sequence 446, App	961	23	100.0	188	10	US-09-774-381-33	Sequence 33, Appli
889	23	100.0	180	15	US-10-157-802-446	Sequence 446, App	962	23	100.0	188	15	US-10-424-599-194934	Sequence 194934,
												US-10-470-390A-34	Sequence 34, Appli

963 23 100.0 190 15 US-10-094-749-3262 Sequence 3262, Ap
964 23 100.0 190 15 US-10-425-114-43126 Sequence 43126, A
965 23 100.0 190 15 US-10-258-662-38 Sequence 38, Appl
966 23 100.0 190 16 US-10-437-963-113668 Sequence 113668,
967 23 100.0 191 16 US-10-437-963-109685 Sequence 109685,
968 23 100.0 191 16 US-10-437-963-166438 Sequence 166438,
969 23 100.0 192 9 US-09-925-300-1469 Sequence 1469, Ap
970 23 100.0 192 15 US-10-264-049-4092 Sequence 4092, Ap
971 23 100.0 192 15 US-10-425-114-41483 Sequence 41483, A
972 23 100.0 192 15 US-10-220-120-236 Sequence 236, App
973 23 100.0 192 16 US-10-343-663A-59 Sequence 59, Appl
974 23 100.0 194 16 US-10-437-963-168567 Sequence 168567,
975 23 100.0 194 16 US-10-767-701-39861 Sequence 39861, A
976 23 100.0 195 15 US-10-424-599-212418 Sequence 212418,
977 23 100.0 196 15 US-10-108-260A-3347 Sequence 3347, Ap
978 23 100.0 196 16 US-10-437-963-128608 Sequence 128608,
979 23 100.0 196 16 US-10-437-963-138191 Sequence 138191,
980 23 100.0 198 9 US-09-738-626-5036 Sequence 5036, Ap
981 23 100.0 198 16 US-10-437-963-135351 Sequence 135351,
982 23 100.0 199 15 US-10-425-114-64324 Sequence 64324, A
983 23 100.0 199 15 US-10-671-403-185 Sequence 185, App
984 23 100.0 199 15 US-10-671-419-185 Sequence 185, App
985 23 100.0 199 15 US-10-670-844-185 Sequence 185, App
986 23 100.0 199 15 US-10-671-134-185 Sequence 185, App
987 23 100.0 199 15 US-10-673-098-185 Sequence 185, App
988 23 100.0 199 15 US-10-672-638-185 Sequence 185, App
989 23 100.0 199 16 US-10-673-127-185 Sequence 185, App
990 23 100.0 199 16 US-10-670-817-185 Sequence 185, App
991 23 100.0 199 16 US-10-673-119-185 Sequence 185, App
992 23 100.0 199 16 US-10-671-207-185 Sequence 185, App
993 23 100.0 199 17 US-10-673-120-185 Sequence 185, App
994 23 100.0 200 15 US-10-282-122A-51631 Sequence 51631, A
995 23 100.0 200 15 US-10-425-114-72600 Sequence 72600, A
996 23 100.0 200 16 US-09-767-701-33617 Sequence 33617, A
997 23 100.0 201 9 US-09-220-920-116 Sequence 116, App
998 23 100.0 201 11 US-09-833-245-1506 Sequence 1506, A
999 23 100.0 201 15 US-10-425-114-66867 Sequence 66867, A
1000 23 100.0 202 14 US-10-012-542-261 Sequence 261, App

ALIGNMENTS

RESULT 1

US-10-197-954-120
; Sequence 120, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: Kuster, Hubert
; APPLICANT: Siddiqi, Subaib
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-197-954-120

Query Match 100.0%; Score 23; DB 14; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
DB 1 GQPR 4
RESULT 2
US-10-742-344-3
; Sequence 3, Application US/10742344
; Publication No. US20040120918A1
; GENERAL INFORMATION:
; APPLICANT: LINTNER, KARL
; APPLICANT: GABRIEL, DENISE E.
; TITLE OF INVENTION: COSMETIC OR DERMOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: OF CERAMIDES AND POLYPEPTIDES
; FILE REFERENCE: SEDERM 3.0-002
; CURRENT APPLICATION NUMBER: US/10/742,344
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: FR 03 05707
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: see specification as filed for detailed description of lipid
; OTHER INFORMATION: group attachments and preferred embodiments
US-10-742-344-3

Query Match 100.0%; Score 23; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 1 GQPR 4

RESULT 3

US-10-731-921-3
; Sequence 3, Application US/10731921
; Publication No. US20040132667A1
; GENERAL INFORMATION:
; APPLICANT: LINTNER, KARL
; TITLE OF INVENTION: COMPOSITIONS CONTAINING MIXTURES OF TETRAPEPTIDES AND TRIPEPTIDES
; FILE REFERENCE: SEDERM 3.0-001
; CURRENT APPLICATION NUMBER: US/10/731,921
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/FR03/03423
; PRIOR FILING DATE: 2003-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: see specification as filed for detailed description of lipid
; OTHER INFORMATION: group attachments and preferred embodiments
US-10-731-921-3

Query Match 100.0%; Score 23; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|
|
|
|
Db 1 GQPR 4

RESULT 4

US-10-760-085-120
; Sequence 120, Application US/10760085
; Publication No. US20050042771A1
; GENERAL INFORMATION:
; APPLICANT: Hubert K'ster
; APPLICANT: Daniel Paul Little
; APPLICANT: Suhaib Mahmood Siddiqi
; APPLICANT: Matthew Peter Grealish
; APPLICANT: Subramaniam Marappan
; APPLICANT: Chester Frederick Haseman III
; APPLICANT: Ping Yip
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2309
; CURRENT APPLICATION NUMBER: US/10/760,085
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 60/441,398
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-760-085-120

Query Match 100.0%; Score 23; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|
|
|
|
Db 1 GQPR 4

RESULT 5

US-09-776-874A-8
; Sequence 8, Application US/09776874A
; Patent No. US20020102560A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 01/22603
; CURRENT APPLICATION NUMBER: US/09/776,874A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-776-874A-8

Query Match 100.0%; Score 23; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|
|
|
|
Db 6 GQPR 9

RESULT 6

US-09-988-113-8
; Sequence 8, Application US/09988113
; Patent No. US20020168749A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
; FILE REFERENCE: 01/22781
; CURRENT APPLICATION NUMBER: US/09/988,113
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 09/776,874
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US09/258,892
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: US 09/109,386
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide derived from tryptic digestion of human heparanase
US-09-988-113-8

Query Match 100.0%; Score 23; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
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|
|
|
Db 6 GQPR 9

RESULT 7

US-10-341-582-8
; Sequence 8, Application US/10341582
; Publication No. US20030161823A1
; GENERAL INFORMATION:
; APPLICANT: Meta Ilan
; APPLICANT: Israel Vlodavsky
; APPLICANT: Oron Yacoby-Zeevi
; APPLICANT: Iris Pecker
; TITLE OF INVENTION: THERAPEUTIC AND COSMETIC USES OF HEPARANASES
; FILE REFERENCE: 25449
; CURRENT APPLICATION NUMBER: US/10/341,582
; CURRENT FILING DATE: 2003-01-14
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide derived from tryptic digestion of human heparanase
US-10-341-582-8

Query Match 100.0%; Score 23; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 6 GQPR 9

RESULT 8

US-10-384-451-8
; Sequence 8, Application US/10384451
; Publication No. US20030170860A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 25718
; CURRENT FILING DATE: 2003-03-10
; CURRENT APPLICATION NUMBER: US/10/384,451
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide derived from tryptic digestion of human heparanase
US-10-384-451-8

Query Match 100.0%; Score 23; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 6 GQPR 9

RESULT 9

US-10-384-450-8
; Sequence 8, Application US/10384450
; Publication No. US20030190737A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 25717
; CURRENT APPLICATION NUMBER: US/10/384,450
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide derived from tryptic digestion of human heparanase
US-10-384-450-8

Query Match 100.0%; Score 23; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 6 GQPR 9

RESULT 10

US-10-371-218A-8

; Sequence 8, Application US/10371218A
; Publication No. US20030217375A1
; GENERAL INFORMATION:

; APPLICANT: Zcharia, Eyal
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Metzger, Shula
; APPLICANT: Pecker, Iris
; APPLICANT: Ilan, Neta
; APPLICANT: Chajek-Shaul, Tova
; APPLICANT: Goldshmidt, Orit
; TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING HEPARANASE AND USES THEREOF
; FILE REFERENCE: 25783
; CURRENT APPLICATION NUMBER: US/10/371,218A
; CURRENT FILING DATE: 2003-07-01
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide derived from tryptic digestion of human heparanase
US-10-371-218A-8

Query Match 100.0%; Score 23; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 6 GQPR 9

RESULT 11

US-10-456-573-8
; Sequence 8, Application US/10456573
; Publication No. US20030236215A1
; GENERAL INFORMATION:
; APPLICANT: Pecker, Iris
; APPLICANT: Vlodavsky, Israel
; APPLICANT: Feinstein, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 25677
; CURRENT APPLICATION NUMBER: US/10/456,573
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: US 09/435,739
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: US 09/258,892
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: PCT/US98/17954
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/922,170
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-456-573-8

Query Match 100.0%; Score 23; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 6 GQPR 9

RESULT 12

US-10-785-116-8

; Sequence 8, Application US/10785116
; Publication No. US2004014247A1
; GENERAL INFORMATION:

; APPLICANT: Pecker, Iris
; APPLICANT: Vlodayevsky, Israel

; APPLICANT: Feinstein, Elena

; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; FILE REFERENCE: 27674

; CURRENT APPLICATION NUMBER: US/10/785,116
; CURRENT FILING DATE: 2004-02-25

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Peptide derived from tryptic digestion of human heparanase
US-10-785-116-8

Query Match 100.0%; Score 23; DB 16; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.3e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 6 GQPR 9

RESULT 13

US-09-920-306-63

; Sequence 63, Application US/09920306

; Publication No. US20040029808A1

; GENERAL INFORMATION:

; APPLICANT: Unilever PLC

; APPLICANT: Unilever NV

; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for

; FILE REFERENCE: Peptide Mimotopes

; CURRENT APPLICATION NUMBER: US/09/920,306

; CURRENT FILING DATE: 2001-08-02

; PRIOR FILING DATE: 2000-08-03

; NUMBER OF SEQ ID NOS: 80

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 63

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide

US-09-920-306-63

Query Match

Best Local Similarity 100.0%; Score 23; DB 11; Length 12;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 5 GQPR 8

RESULT 14

US-09-989-920-263

; Sequence 263, Application US/09989920

; Patent No. US20020172957A1

; GENERAL INFORMATION:

; APPLICANT: Macina, Roberto

; APPLICANT: Recipon, Herve

; APPLICANT: Chen, Sei-Yu

; APPLICANT: Sun, Yongming

; APPLICANT: Liu, Chenghua

; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot

; FILE REFERENCE: DEX-0291

; CURRENT APPLICATION NUMBER: US/09/989,920

; CURRENT FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: 60/252,500

; PRIOR FILING DATE: 2000-11-22

; NUMBER OF SEQ ID NOS: 284

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 263

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-989-920-263

Query Match

Best Local Similarity 100.0%; Score 23; DB 9; Length 13;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 3 GQPR 6

RESULT 15

US-09-873-637-3

; Sequence 3, Application US/09873637

; Patent No. US20020061543A1

; GENERAL INFORMATION:

; APPLICANT: Ross, Jeffrey

; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN

; FILE REFERENCE: 960296.95131

; CURRENT APPLICATION NUMBER: US/09/873,637

; CURRENT FILING DATE: 2001-06-04

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-873-637-3

Query Match

Best Local Similarity 100.0%; Score 23; DB 9; Length 14;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 9 GQPR 12

RESULT 16

US-10-327-598-226

; Sequence 226, Application US/10327598

; Publication No. US20040181039A1

; GENERAL INFORMATION:

; APPLICANT: Krah, Eugene

; APPLICANT: Guo, Honliang

; APPLICANT: Aiyappa, Ashok

; APPLICANT: Lawton, Robert

; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and

; FILE REFERENCE: 01-799-A

; CURRENT APPLICATION NUMBER: US/10/327,598

; CURRENT FILING DATE: 2002-12-20

; PRIOR APPLICATION NUMBER: US 60/344,874

; PRIOR FILING DATE: 2001-12-21

; NUMBER OF SEQ ID NOS: 1139

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 226

; LENGTH: 15

; TYPE: PRT

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; ORGANISM: canis familiaris;
US-10-327-598-226

Query Match      100.0%; Score 23; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      11 GQPR 14

RESULT 17
US-09-984-017-2
; Sequence 2, Application US/09984017
; Patent No. US20020115614A1
; GENERAL INFORMATION:
; APPLICANT: FRANK, MICHAEL M.
; APPLICANT: JIANG, HAIXIANG J.
; TITLE OF INVENTION: INHIBITION OF COMPLEMENT ACTION
; FILE REFERENCE: 1579-619
; CURRENT APPLICATION NUMBER: US/09/984,017
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US00/10928
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/130,936
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CH2 or CH3 domain of IgG
US-09-984-017-2

Query Match      100.0%; Score 23; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      8 GQPR 11

RESULT 18
US-10-408-765A-3069
; Sequence 3069, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenna, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3069
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide containing doubly oxidized tryptophan
; OTHER INFORMATION: (N-formylkynurenine) from the human cardiac
; OTHER INFORMATION: proteome.
```

```
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 2,7
; OTHER INFORMATION: Xaa = N-formylkynurenine
US-10-408-765A-3069

Query Match      100.0%; Score 23; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      15 GQPR 18

RESULT 19
US-09-843-676-194
; Sequence 194, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-09-843-676-194

Query Match      100.0%; Score 23; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|
|
|
|
Db 15 GQPR 18

RESULT 20
US-09-438-486-194
; Sequence 194, Application US/09438486
; Publication No. US2003009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US2003009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-438-486-194

Query Match 100.0%; Score 23; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|
|
|
|
Db 15 GQPR 18

RESULT 21
US-10-053-758-194
; Sequence 194, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-10-053-758-194

Query Match 100.0%; Score 23; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|
|
|
|
Db 15 GQPR 18

RESULT 22

US-10-054-295-194
; Sequence 194, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-10-054-295-194
Query Match 100.0%; Score 23; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 15 GQPR 18
RESULT 23
US-10-054-611-194
; Sequence 194, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor

US-10-054-295-194
; Sequence 194, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-10-054-295-194
Query Match 100.0%; Score 23; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 15 GQPR 18
RESULT 24
US-10-325-810-313
; Sequence 313, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor

NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 313:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 313:
US-10-325-810-313

Query Match 100.0%; Score 23; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 15 GQPR 18

RESULT 25

US-10-877-146-313
Sequence 313, Application US/10877146
Publication No. US20050013825A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,146
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 313:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 313:
US-10-877-146-313

Query Match 100.0%; Score 23; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
DB 15 GQPR 18

RESULT 26

US-10-263-162-45
Sequence 45, Application US/10263162
Publication No. US2003018686A1
GENERAL INFORMATION:
APPLICANT: Rosenbaum, et al.
TITLE OF INVENTION: Anti-Angiogenic Peptides

; FILE REFERENCE: REG 810
; CURRENT APPLICATION NUMBER: US/10/263,162
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/326,712
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 22
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-263-162-45

Query Match 100.0%; Score 23; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 8 GQPR 11

RESULT 27
US-10-384-060-15
; Sequence 15, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Honayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide able to nonspecifically activate lymphocytes
US-10-384-060-15

Query Match 100.0%; Score 23; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 7 GQPR 10

RESULT 28
US-09-847-102A-119
; Sequence 119, Application US/09847102A
; Publication No. US2003004409A1
; GENERAL INFORMATION:
; APPLICANT: University of California
; APPLICANT: Carson, Dennis A.
; APPLICANT: Cort, Maribat
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Lorenzo, Leon M.
; APPLICANT: Malini, Sen
; TITLE OF INVENTION: IMMUNOLOGIC COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: STUDYING AND TREATING CANCERS EXPRESSING FRIZZLED ANTIGENS
; FILE REFERENCE: 22600-20629-00
; CURRENT APPLICATION NUMBER: US/09/847,102A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-102A-119

Query Match 100.0%; Score 23; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 20 GQPR 23

RESULT 29
US-09-820-843A-81
; Sequence 81, Application US/09820843A
; Publication No. US20030039963A1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
; TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
; FILE REFERENCE: Q63915
; CURRENT APPLICATION NUMBER: US/09/820,843A
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 81
; LENGTH: 27
; TYPE: PRT
; ORGANISM: M. tuberculosis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: hypothetical protein Rv1572c
; NAME/KEY: misc feature
; OTHER INFORMATION: gi|2117265
US-09-820-843A-81

Query Match 100.0%; Score 23; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 2 GQPR 5

RESULT 30
US-10-029-386-28116
; Sequence 28116, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28116
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens


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/ FEATURE:
/ OTHER INFORMATION: MAP TO CHR21 64.0
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.87
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.93
/ OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.8
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
/ OTHER INFORMATION: SWISSPROT HIT: P21483, EVALUAE 3.90e+00
US-10-029-386-28116

Query Match      100.0%; Score 23; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      28 GQPR 31

RESULT 31
US-10-295-732-2
; Sequence 2, Application US/10295732
; Publication No. US20030104569A1
; GENERAL INFORMATION:
; APPLICANT: Oritani, Kenji
; APPLICANT: Tomiyama, Yoshiaki
; APPLICANT: Matsuzawa, Yuji
; APPLICANT: Kincaide, Paul W.
; TITLE OF INVENTION: Proteins Suppressing proliferation of lympho-hematopoietic cells
; FILE REFERENCE: SHIM-003DIV
; CURRENT APPLICATION NUMBER: US/10/295,732
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 09/523,686
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: JP 11/107246
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRP
; ORGANISM: Mus musculus
US-10-295-732-2

Query Match      100.0%; Score 23; DB 14; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      13 GQPR 16

RESULT 32
US-10-437-963-130130
; Sequence 130130, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
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/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 130130
/ LENGTH: 34
/ TYPE: PRP
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_32320C.1.pep
US-10-437-963-130130

Query Match      100.0%; Score 23; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      1 GQPR 4

RESULT 33
US-10-038-612-70
; Sequence 70, Application US/10038612
; Publication No. US20020160478A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: Short Peptides Which Selectively
; FILE REFERENCE: 1242,1029-000 (CMCC-679)
; CURRENT APPLICATION NUMBER: US/10/038,612
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 35
; TYPE: PRP
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: TrkC
US-10-038-612-70

Query Match      100.0%; Score 23; DB 13; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      26 GQPR 29

RESULT 34
US-10-231-417-404
; Sequence 404, Application US/10231417
; Publication No. US20030176681A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 148 Human Secreted Proteins
; FILE REFERENCE: PZ019P1
; CURRENT APPLICATION NUMBER: US/10/231,417
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US/09/296,622
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 619
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 404
; LENGTH: 35
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-231-417-404

Query Match      100.0%; Score 23; DB 14; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 GQPR 4
Db      3 GQPR 6

RESULT 35
US-09-104-750-50
; Sequence 50, Application US/09104750
; Publication No. US20030104364A1
; GENERAL INFORMATION:
; APPLICANT: Russell, John
; APPLICANT: Colpitts, Tracey
; TITLE OF INVENTION: Methods and Reagents Useful
; TITLE OF INVENTION: for Detecting Disease of the Breast
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,750
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 6121.US.01
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6121.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20030104364A1e
US-09-104-750-50

Query Match      100.0%; Score 23; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      19 GQPR 22

RESULT 36
US-10-437-963-108727
; Sequence 108727, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

Query Match      100.0%; Score 23; DB 16; Length 36;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      32 GQPR 35

RESULT 37
US-10-767-701-61720
; Sequence 61720, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 61720
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 9850456.pep
US-10-767-701-61720

Query Match      100.0%; Score 23; DB 16; Length 36;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      32 GQPR 35

RESULT 38
US-10-012-542-262
; Sequence 262, Application US/10012542
; Publication No. US20030044851A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 262
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-542-262

Query Match 100.0%; Score 23; DB 14; Length 37;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 16 GQPR 19

RESULT 39
US-10-115-123-262
; Sequence 262, Application US/10115123
; Publication No. US20030065151A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: PZ029G30AP1D2
; CURRENT APPLICATION NUMBER: US/10/115,123
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 262
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-123-262

Query Match 100.0%; Score 23; DB 14; Length 37;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 16 GQPR 19

RESULT 40
US-09-776-724A-227
; Sequence 227, Application US/09776724A
; Publication No. US20030050455A1
; GENERAL INFORMATION:
; APPLICANT: Rozen et al.
; TITLE OF INVENTION: 64 Human Secreted Proteins
; FILE REFERENCE: PZ011
; CURRENT APPLICATION NUMBER: US/09/776,724A

; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/180,909
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 09/669,688
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/229,982
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: PCT/US98/14613
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/052,661
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,872
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,871
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,874
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,873
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,870
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/052,875
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: 60/053,440
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,441
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,442
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/056,359
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,725
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,985
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,952
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,989
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,361
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,726
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,724
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,946
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,683
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 227
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-776-724A-227

Query Match 100.0%; Score 23; DB 10; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 35 GQPR 38

RESULT 41
US-10-437-963-152267
; Sequence 152267, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

```
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 152267
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52335C.1.pap
US-10-437-963-152267

Query Match          100.0%; Score 23; DB 16; Length 38;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      6 GQPR 9

RESULT 42
US-10-437-963-151924
; Sequence 151924, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 151924
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52022C.1.pap
US-10-437-963-151924

Query Match          100.0%; Score 23; DB 16; Length 40;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      2 GQPR 5

RESULT 43
US-09-864-761-45995
; Sequence 45995, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
```

```
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45995
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008567.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
; OTHER INFORMATION: SWISSPROT HIT: P55067, EVALUATE 8.30e+00
; OTHER INFORMATION: EST_HUMAN HIT: BF125921.1, EVALUATE 8.00e-08
US-09-864-761-45995

Query Match          100.0%; Score 23; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      12 GQPR 15

RESULT 44
US-10-240-145-162
; Sequence 162, Application US/10240145
; Publication No. US20030235883A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
```

; FILE REFERENCE: 21272-048
; CURRENT APPLICATION NUMBER: US/10/240,145
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/668,680
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/695,618
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 09/728,711
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 2000-YET ASSIGNED
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: Custom
; SEQ ID NO 162
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(41)
; OTHER INFORMATION: xaa = X or * as defined in Table 6
US-10-240-145-162

Query Match 100.0%; Score 23; DB 15; Length 41;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 29 GQPR 32

RESULT 45
US-10-424-599-145097
; Sequence 145097, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 145097
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_102040C.1.pap
US-10-424-599-145097

Query Match 100.0%; Score 23; DB 15; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 13 GQPR 16

RESULT 46
US-10-424-599-177895
; Sequence 177895, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 177895
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(44)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131655C.1.pap
US-10-424-599-177895

Query Match 100.0%; Score 23; DB 15; Length 44;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 31 GQPR 34

RESULT 47
US-10-424-599-255629
; Sequence 255629, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 255629
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_72854C.1.pap
US-10-424-599-255629

Query Match 100.0%; Score 23; DB 15; Length 44;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 40 GQPR 43

RESULT 48
US-09-864-761-38712
; Sequence 38712, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anncmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38712
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL022319.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 17
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5
; OTHER INFORMATION: EST_HUMAN HIT: T85631.1, EVALUATE 5.208+00

Query Match 100.0%; Score 23; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 10 GQPR 13

RESULT 49

US-10-437-963-139079
; Sequence 139079, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 139079
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_40406C.1.pap
US-10-437-963-139079

Query Match 100.0%; Score 23; DB 16; Length 46;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 21 GQPR 24

RESULT 50

US-09-864-761-45670
; Sequence 45670, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45670
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009699.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.81
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.97
; OTHER INFORMATION: SWISSPROT HIT: Q00706, EVALUE 4.70e+00
; OTHER INFORMATION: EST_HUMAN HIT: BE777699.1, EVALUE 1.30e+00
US-09-864-761-45670

Query Match 100.0%; Score 23; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 19 GQPR 22

RESULT 51

US-09-864-761-48301
; Sequence 48301, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48301
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009181.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
; OTHER INFORMATION: EST_HUMAN HIT: AUI42410.1, EVALUE 1.00e-11
US-09-864-761-48301

Query Match 100.0%; Score 23; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 11 GQPR 14

RESULT 52

US-09-864-408A-8876
; Sequence 8876, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encor
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8876
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-8876

Query Match 100.0%; Score 23; DB 11; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 20 GQPR 23

RESULT 53

US-10-091-007-26
; Sequence 26, Application US/10091007
; Publication No. US20030170782A1
; GENERAL INFORMATION:
; APPLICANT: Microbial
; APPLICANT: Le Page, Richard W F
; APPLICANT: Hanniffy, Sean B
; APPLICANT: Wells, Jeremy M

```
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21978WO
; CURRENT APPLICATION NUMBER: US/10/091,007
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: GB 9921125.2
; PRIOR FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-091-007-26

Query Match          100.0%; Score 23; DB 14; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      16 GQPR 19

RESULT 54
US-10-424-599-185208
; Sequence 185208, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 185208
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: unsure
; LOCATION: (1)..(51)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_138257C.1.pap
US-10-424-599-185208

Query Match          100.0%; Score 23; DB 15; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      17 GQPR 20

RESULT 55
US-10-424-599-180797
; Sequence 180797, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
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; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 180797
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_134274C.1.pap
US-10-424-599-180797

Query Match          100.0%; Score 23; DB 15; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      15 GQPR 18

RESULT 56
US-10-424-599-247027
; Sequence 247027, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 247027
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65095C.1.pap
US-10-424-599-247027

Query Match          100.0%; Score 23; DB 15; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
Db      32 GQPR 35

RESULT 57
US-10-424-599-170629
; Sequence 170629, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 170629
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_125093C.1.pap
US-10-424-599-170629
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Query Match      100.0%; Score 23; DB 15; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      16 GQPR 19

RESULT 58
US-10-424-599-151840
; Sequence 151840, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 151840
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_108135C.1.pep
US-10-424-599-151840

Query Match      100.0%; Score 23; DB 15; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      14 GQPR 17

RESULT 59
US-10-029-386-34129
; Sequence 34129, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34129
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004624.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.46
; OTHER INFORMATION: SWISSPROT HIT: Q04781, EVALU8 8.10e+00
US-10-029-386-34129

Query Match      100.0%; Score 23; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      2 GQPR 5
```

```
RESULT 60
US-10-437-963-155414
; Sequence 155414, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 155414
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_5517C.1.pep
US-10-437-963-155414

Query Match      100.0%; Score 23; DB 16; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      16 GQPR 19

RESULT 61
US-09-864-408A-6778
; Sequence 6778, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6778
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Homo sapiens
US-09-864-408A-6778

Query Match      100.0%; Score 23; DB 11; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      8 GQPR 11

RESULT 62
US-10-424-599-181996
; Sequence 181996, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
```

```
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 181996
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_135356C.1.pep
US-10-424-599-181996

Query Match      100.0%; Score 23; DB 15; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      1 GQPR 4

RESULT 63
US-10-424-599-145320
; Sequence 145320, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 145320
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_102243C.1.pep
US-10-424-599-145320

Query Match      100.0%; Score 23; DB 15; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      10 GQPR 13

RESULT 64
US-10-424-599-155931
; Sequence 155931, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
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; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 155931
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_111826C.1.pep
US-10-424-599-155931

Query Match      100.0%; Score 23; DB 15; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      35 GQPR 38

RESULT 65
US-09-864-408A-5620
; Sequence 5620, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5620
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-5620

Query Match      100.0%; Score 23; DB 11; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      21 GQPR 24

RESULT 66
US-10-424-599-177632
; Sequence 177632, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 177632
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131417C.1.pep
US-10-424-599-177632

Query Match      100.0%; Score 23; DB 15; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

||||

Db 27 GQPR 30

RESULT 67

US-10-424-599-233719
; Sequence 233719, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 233719

; LENGTH: 63

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_53073C.1.pap

US-10-424-599-233719

Query Match

Best Local Similarity 100.0%; Score 23; DB 15; Length 63;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

||||

Db 36 GQPR 39

RESULT 68

US-10-437-963-163011
; Sequence 163011, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 163011

; LENGTH: 64

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_62046C.1.pap

US-10-437-963-163011

Query Match

Best Local Similarity 100.0%; Score 23; DB 16; Length 64;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

||||

Db 2 GQPR 5

RESULT 69

US-10-437-963-155904
; Sequence 155904, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 155904

; LENGTH: 65

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_55623C.1.pap

US-10-437-963-155904

Query Match

Best Local Similarity 100.0%; Score 23; DB 16; Length 65;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

||||

Db 24 GQPR 27

RESULT 70

US-10-437-963-104594
; Sequence 104594, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 104594

; LENGTH: 67

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_101913C.1.pap

US-10-437-963-104594

Query Match

Best Local Similarity 100.0%; Score 23; DB 16; Length 67;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

||||

Db 28 GQPR 31

RESULT 71

US-09-864-408A-6184
; Sequence 6184, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encoded by
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6184
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-6184

Query Match 100.0%; Score 23; DB 11; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 45 GQPR 48

RESULT 72

US-10-105-004-139
; Sequence 139, Application US/10105004
; Publication No. US20030105002A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Jeffrey
; Semina, Elena
; TITLE OF INVENTION: RIEG COMPOSITIONS AND THERAPEUTIC
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/105,004
; FILING DATE: 22-Mar-2002
; APPLICATION DATA:
; APPLICATION NUMBER: US/08/754,477
; FILING DATE: 22-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIA-022.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 139:

US-10-105-004-139

Query Match 100.0%; Score 23; DB 14; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 42 GQPR 45

RESULT 73

US-10-437-963-106825
; Sequence 106825, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106825
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT4530_11234C.1.pap
US-10-437-963-106825

Query Match 100.0%; Score 23; DB 16; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 55 GQPR 58

RESULT 74

US-10-424-599-143493
; Sequence 143493, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 143493
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(70)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT3847_100589C.1.pap
US-10-424-599-143493

Query Match 100.0%; Score 23; DB 15; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|
|
|
|
Db 43 GQPR 46

RESULT 75
US-10-424-599-211412
; Sequence 211412, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 211412
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_32931C.1.pep
US-10-424-599-211412

Query Match 100.0%; Score 23; DB 15; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|
|
|
|
Db 53 GQPR 56

Search completed: May 17, 2005, 10:10:47
Job time : 148 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2005, 09:58:31 ; Search time 169 Seconds
(without alignments)
9.154 Million cell updates/sec

Title: US-10-731-921-3

Perfect score: 23

Sequence: 1 GQPR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	4	3	AAB07766
2	23	100.0	4	4	AAB92377
3	23	100.0	4	7	ADJ81639
4	23	100.0	4	8	ADN03394
5	23	100.0	4	8	ADQ93809
6	23	100.0	4	8	ADR03553
7	23	100.0	4	8	ADR42229
8	23	100.0	9	2	AAV02344
9	23	100.0	9	3	AAB08848
10	23	100.0	9	7	ADG88798
11	23	100.0	9	8	ADL16377
12	23	100.0	9	8	ADM48714
13	23	100.0	10	2	AAV34181
14	23	100.0	10	2	AAV17071
15	23	100.0	11	1	AAP60496
16	23	100.0	11	6	ABU03391
17	23	100.0	11	7	ADD23535
18	23	100.0	12	5	AAU87007
19	23	100.0	13	1	AAP51019
20	23	100.0	13	5	ABU60996
21	23	100.0	14	4	AAW98739
22	23	100.0	15	1	AAP82447
23	23	100.0	15	2	AAV13277
24	23	100.0	15	2	AAV13300
25	23	100.0	15	2	AAV13251

26	23	100.0	15	7	ADM08091
27	23	100.0	15	7	ADM07959
28	23	100.0	16	6	ABP55617
29	23	100.0	17	3	AAB36861
30	23	100.0	18	2	AAR49648
31	23	100.0	18	2	AAR49647
32	23	100.0	18	2	AAR49646
33	23	100.0	18	2	AAR49534
34	23	100.0	18	2	AAR49533
35	23	100.0	18	2	AAR49532
36	23	100.0	22	6	ABR57545
37	23	100.0	23	1	AAP30407
38	23	100.0	23	1	AAP30405
39	23	100.0	23	1	AAP30404
40	23	100.0	23	1	AAP30406
41	23	100.0	23	1	AAP30409
42	23	100.0	23	8	ADH89371
43	23	100.0	23	8	ADH89371
44	23	100.0	24	1	ADH89371
45	23	100.0	24	1	ADH89371
46	23	100.0	27	7	ABO23580
47	23	100.0	28	2	AAW37936
48	23	100.0	28	3	AAV56879
49	23	100.0	31	8	ABO54482
50	23	100.0	33	4	ABO54482
51	23	100.0	35	2	AAV19644
52	23	100.0	35	3	AAV98355
53	23	100.0	35	4	AAW82815
54	23	100.0	35	5	AAU83474
55	23	100.0	36	7	ABW00600
56	23	100.0	37	3	AAW86343
57	23	100.0	37	6	ABO53488
58	23	100.0	38	2	ABO23432
59	23	100.0	38	8	ADR20820
60	23	100.0	39	2	AAW25684
61	23	100.0	40	8	ADP45479
62	23	100.0	41	4	AAU68589
63	23	100.0	41	4	AAW37357
64	23	100.0	41	4	AAW91448
65	23	100.0	41	4	AAW64399
66	23	100.0	41	4	ABG58845
67	23	100.0	42	5	ABG80821
68	23	100.0	42	8	ADH97549
69	23	100.0	43	2	AAW95499
70	23	100.0	43	4	ABG26421
71	23	100.0	43	5	AAW21238
72	23	100.0	43	7	ADH21604
73	23	100.0	44	4	AAW89537
74	23	100.0	44	4	AAO03183
75	23	100.0	46	4	AAW19030
76	23	100.0	46	4	ABG38236
77	23	100.0	46	4	ABG38236
78	23	100.0	46	4	AAW31669
79	23	100.0	46	4	ABG23414
80	23	100.0	46	4	AAW71387
81	23	100.0	46	4	AAW58864
82	23	100.0	46	4	ABG53089
83	23	100.0	46	5	ABG41188
84	23	100.0	47	2	AAW95034
85	23	100.0	49	4	AAU01054
86	23	100.0	49	4	ABG42912
87	23	100.0	49	4	AAW36732
88	23	100.0	49	4	AAW76627
89	23	100.0	49	4	AAW63813
90	23	100.0	49	5	ABG58321
91	23	100.0	50	4	ABG45854
92	23	100.0	50	4	AAW38222
93	23	100.0	50	4	AAW78006
94	23	100.0	50	4	AAU39742
95	23	100.0	50	5	ABG47019
96	23	100.0	50	5	ABF35465
97	23	100.0	50	5	AAW50385
98	23	100.0	50	5	ADR41540

Adm08091	Canine im
Adm07959	Canine im
Abp55617	Human cyt
Aab36861	Residue
Aar49648	Sequence
Aar49647	Sequence
Aar49646	Sequence
Aar49534	Human Ig
Aar49533	Human Ig
Aar49532	Human Ig
AbR57545	Anti-angi
Aap30407	Sequence
Aap30405	Sequence
Aap30404	Sequence
Aap30406	Sequence
Aap30409	Sequence
Adh89371	Human tra
Adh89371	Dementia
Adh89371	Dementia
Aap30413	Sequence
Aau89298	Insulin/i
Abo23580	Mycobacte
Aaw37936	Herpes vi
Aay56879	Peptide i
AbO54482	Human gen
AbS1356	Mouse blo
Aay19644	SEQ ID NO
Aay98355	Alpha D p
Aaw82815	Human imm
Aau83474	Human pho
Abw00600	BS136 epi
Aay86343	Human gen
AbO53488	Novel hum
Abo23432	Amino aci
Adr20820	Human sec
Aar25684	Exon VII
Adp45479	Human col
Aau68589	Human nov
Aam37357	Peptide #
Aam91448	Human imm
Aam64399	Human bra
Abg58845	Human liv
Abg80821	Rat Sp-A
Adh97549	Dementia
Aar95499	E85, mono
Abg26421	Novel hum
Aae21238	Human gen
Adi21604	Novel hum
Adi21603	Novel hum
Aam89537	Human imm
Aao03183	Human pol
Aam19030	Peptide #
Abb38236	Peptide #
Aam31669	Peptide #
Abb23414	Protein #
Aam71387	Human bon
Aam58864	Human bra
Abg53089	Human liv
Abg41188	Human pep
Aau95034	Fragment
Aau01054	Human sec
Abb42912	Peptide #
Aam36732	Peptide #
Aam76627	Human bon
Aam63813	Human bra
Abg58321	Human liv
Abg45854	Human pep
Aam38222	Peptide #
Aam78006	Human bon
Aau39742	Propionib
Abg47019	Human pep
Abp35465	Human ORF
Aam50385	Mouse hep
Adr41540	Human CD-

99	23	100.0	50	6	ABM36261	Abm36261 Propionib	172	23	100.0	68	4	AAU54837	Aau54837 Propionib
100	23	100.0	51	4	AAU53376	Aau53376 Propionib	173	23	100.0	68	5	ABF34119	Abp34119 Human ORF
101	23	100.0	51	4	AAU51468	Aau51468 Propionib	174	23	100.0	68	6	ABM51356	Abm51356 Propionib
102	23	100.0	51	4	AAU51512	Aau51512 Propionib	175	23	100.0	68	7	ABO07413	Abm07413 Human RIE
103	23	100.0	51	4	AAU64415	Aau64415 Propionib	176	23	100.0	68	7	ADH83479	Adh83479 RGD/Solur
104	23	100.0	51	4	AAU03613	Aau03613 Group B S	177	23	100.0	68	8	ADK01862	Adk01862 Hepatitis
105	23	100.0	51	5	ABP04226	Abp04226 Human ORF	178	23	100.0	69	4	ABB70463	Abb70463 Drosophila
106	23	100.0	51	6	ABM60934	Abm60934 Propionib	179	23	100.0	69	4	ABU50004	Abu50004 Propionib
107	23	100.0	51	6	ABM47987	Abm47987 Propionib	180	23	100.0	69	5	ABP06441	Abp06441 Human ORF
108	23	100.0	51	6	ABM51895	Abm51895 Propionib	181	23	100.0	69	5	ADK34226	Adk34226 Novel hum
109	23	100.0	51	6	ABM48031	Abm48031 Propionib	182	23	100.0	69	6	ABM51523	Abm51523 Propionib
110	23	100.0	53	4	AAU68680	Aau68680 Human imm	183	23	100.0	70	4	AU50626	Au50626 Propionib
111	23	100.0	53	7	ADH62382	Adh62382 Rhizomuc	184	23	100.0	70	6	ABM47145	Abm47145 Propionib
112	23	100.0	54	4	AAU55625	Aau55625 Propionib	185	23	100.0	71	4	AAU94044	Aau94044 Human rep
113	23	100.0	54	6	ABM52144	Abm52144 Propionib	186	23	100.0	71	4	AAU55545	Aau55545 Propionib
114	23	100.0	55	4	AAU50648	Aau50648 Propionib	187	23	100.0	71	6	ABM52064	Abm52064 Propionib
115	23	100.0	55	4	AAU58126	Aau58126 Propionib	188	23	100.0	72	4	AAU41006	Aau41006 Propionib
116	23	100.0	55	4	AAU40074	Aau40074 Propionib	189	23	100.0	72	4	AAU31079	Aau31079 Novel hum
117	23	100.0	55	6	ABM36593	Abm36593 Propionib	190	23	100.0	72	6	ABM37525	Abm37525 Propionib
118	23	100.0	55	6	ABM47167	Abm47167 Propionib	191	23	100.0	72	8	ABO58681	Abm58681 Human gen
119	23	100.0	55	6	ABM54645	Abm54645 Propionib	192	23	100.0	73	4	AAU62030	Aau62030 Propionib
120	23	100.0	55	8	ABO60495	Abm60495 Human gen	193	23	100.0	73	4	ABG1663	Abg1663 Propionib
121	23	100.0	56	4	AAU41744	Aau41744 Propionib	194	23	100.0	73	4	ABG17830	Abg17830 Novel hum
122	23	100.0	56	6	ABM38263	Abm38263 Propionib	195	23	100.0	73	6	ABM58182	Abm58182 Propionib
123	23	100.0	57	4	AAO02186	Aao02186 Human pol	196	23	100.0	73	6	ABM58549	Abm58549 Propionib
124	23	100.0	57	4	AAU42779	Aau42779 Propionib	197	23	100.0	74	2	AAU02663	Aau02663 Human sec
125	23	100.0	57	4	AAU44783	Aau44783 Propionib	198	23	100.0	74	4	ABM87383	Abm87383 Human gen
126	23	100.0	57	4	AAU65234	Aau65234 Propionib	199	23	100.0	74	4	AAU82713	Aau82713 Human imm
127	23	100.0	57	6	ABM39298	Abm39298 Propionib	200	23	100.0	74	4	AAU52503	Aau52503 Propionib
128	23	100.0	57	6	ABM61753	Abm61753 Propionib	201	23	100.0	74	4	AAU55521	Aau55521 Propionib
129	23	100.0	57	6	ABM41302	Abm41302 Propionib	202	23	100.0	74	5	ABG65379	Abg65379 Human alb
130	23	100.0	58	4	AAU67240	Aau67240 Propionib	203	23	100.0	74	6	ABM52040	Abm52040 Propionib
131	23	100.0	58	4	AAU33389	Aau33389 Propionib	204	23	100.0	74	6	ABM49022	Abm49022 Propionib
132	23	100.0	58	5	ABP09132	Abp09132 Human ORF	205	23	100.0	74	7	ADA07342	Ada07342 Human sec
133	23	100.0	58	5	ABP34416	Abp34416 Human ORF	206	23	100.0	74	8	ADL78646	Adl78646 Albumin f
134	23	100.0	58	6	ABU09599	Abu09599 Human cyt	207	23	100.0	74	8	ADN41084	Adn41084 Novel hum
135	23	100.0	58	6	ABM49908	Abm49908 Propionib	208	23	100.0	74	8	ABO55223	Abm55223 Human gen
136	23	100.0	58	6	ABM63759	Abm63759 Propionib	209	23	100.0	75	7	ADH72462	Adh72462 Human end
137	23	100.0	59	4	AAU56513	Aau56513 Propionib	210	23	100.0	75	7	AAU42470	Aau42470 Propionib
138	23	100.0	59	4	AAU39984	Aau39984 Propionib	211	23	100.0	76	6	ABM38989	Abm38989 Propionib
139	23	100.0	59	6	ABM33032	Abm33032 Propionib	212	23	100.0	77	4	AAU53862	Aau53862 Propionib
140	23	100.0	59	6	ABM36503	Abm36503 Propionib	213	23	100.0	77	5	ABP34427	Abp34427 Human ORF
141	23	100.0	59	8	ADH97548	Adh97548 Dementia	214	23	100.0	77	6	ABM50381	Abm50381 Propionib
142	23	100.0	60	2	AAU60318	Aau60318 Human end	215	23	100.0	78	3	AGI19072	Ag19072 Zea may
143	23	100.0	60	4	AAU90064	Aau90064 Human imm	216	23	100.0	78	4	AAU53653	Aau53653 Propionib
144	23	100.0	60	4	AAU83999	Aau83999 Human imm	217	23	100.0	78	4	AAU41173	Aau41173 Propionib
145	23	100.0	60	4	AAU51911	Aau51911 Propionib	218	23	100.0	78	4	AAU30416	Aau30416 Novel hum
146	23	100.0	60	6	ABM48430	Abm48430 Propionib	219	23	100.0	78	6	ABM50172	Abm50172 Propionib
147	23	100.0	60	6	ABM64761	Abm64761 Propionib	220	23	100.0	78	6	ABM37692	Abm37692 Propionib
148	23	100.0	60	7	ABO61526	Abm61526 Klebsiell	221	23	100.0	79	4	AAU58510	Aau58510 Propionib
149	23	100.0	61	8	ADG22289	Adg22289 Cyanophag	222	23	100.0	79	6	ABM55029	Abm55029 Propionib
150	23	100.0	62	4	AAU46690	Aau46690 Propionib	223	23	100.0	80	4	AAU62784	Aau62784 Propionib
151	23	100.0	62	4	AAU51796	Aau51796 Propionib	224	23	100.0	80	4	ABH15979	Abh15979 Human ner
152	23	100.0	62	4	AAU06281	Aau06281 Human foe	225	23	100.0	80	6	ABM59303	Abm59303 Propionib
153	23	100.0	62	5	ABP33837	Abp33837 Human ORF	226	23	100.0	81	4	ABM50101	Abm50101 Human bra
154	23	100.0	62	6	ABU10042	Abu10042 Human cyt	227	23	100.0	81	4	ABG01739	Abg01739 Novel hum
155	23	100.0	62	6	ABM48315	Abm48315 Propionib	228	23	100.0	82	4	AAU71270	Aau71270 Human gen
156	23	100.0	62	6	ABM43209	Abm43209 Propionib	229	23	100.0	82	4	AAU78973	Aau78973 Human pro
157	23	100.0	62	6	ABM65776	Abm65776 Propionib	230	23	100.0	82	4	AAU53683	Aau53683 Propionib
158	23	100.0	63	4	AAU44071	Aau44071 Propionib	231	23	100.0	82	4	AAU63785	Aau63785 Propionib
159	23	100.0	63	6	AAU09600	Abu09600 Human cyt	232	23	100.0	82	4	AAU43502	Aau43502 Propionib
160	23	100.0	63	6	ABM40590	Abm40590 Propionib	233	23	100.0	82	4	ABG05988	Abg05988 Novel hum
161	23	100.0	64	4	ABG08148	Abg08148 Novel hum	234	23	100.0	82	5	ABM83796	Abm83796 Human cal
162	23	100.0	65	4	AAU47579	Aau47579 Propionib	235	23	100.0	82	5	ABG63449	Abg63449 Human alb
163	23	100.0	65	6	ABM44098	Abm44098 Propionib	236	23	100.0	82	6	ADA57560	Ada57560 Human sec
164	23	100.0	67	4	AAU67187	Aau67187 Propionib	237	23	100.0	82	6	ABM60304	Abm60304 Propionib
165	23	100.0	67	4	AAU64827	Aau64827 Propionib	238	23	100.0	82	6	ABM50202	Abm50202 Propionib
166	23	100.0	67	4	AAU43201	Aau43201 Propionib	239	23	100.0	82	6	ABM40021	Abm40021 Propionib
167	23	100.0	67	4	ABM17351	Abm17351 Human ner	240	23	100.0	82	6	ADA41454	Ada41454 Human sec
168	23	100.0	67	5	ABP04739	Abp04739 Human ORF	241	23	100.0	82	7	ADH74575	Adh74575 Human sec
169	23	100.0	67	6	ABM63706	Abm63706 Propionib	242	23	100.0	82	8	ADL76714	Adl76714 Albumin f
170	23	100.0	67	6	ABM61346	Abm61346 Propionib	243	23	100.0	82	8	ABO55288	Abm55288 Human gen
171	23	100.0	67	6	ABM39720	Abm39720 Propionib	244	23	100.0	83	3	AAU41117	Aau41117 Zea may

245	23	100.0	83	4	AAM95977	Aam95977 Human rep	318	23	100.0	107	2	AAR67439	Aar67439 OKT3 mono
246	23	100.0	83	4	ABB96508	Abb96508 Human tes	319	23	100.0	107	3	AG22650	Ag22650 Zee may
247	23	100.0	84	3	ABG35192	Abg35192 Zee may	320	23	100.0	107	4	AU40683	Au40683 Propionib
248	23	100.0	85	7	ADN11806	Adn11806 c-Fps SH2	321	23	100.0	107	5	ABP41236	Abp41236 Human ova
249	23	100.0	86	4	AAM92636	Aam92636 Human dig	322	23	100.0	107	6	ABM37202	Abm37202 Propionib
250	23	100.0	86	4	AAU52558	Aau52558 Propionib	323	23	100.0	107	7	ADD25814	Add25814 Binding d
251	23	100.0	86	4	AAU22630	Aau22630 Novel hum	324	23	100.0	107	7	ADD25815	Add25815 Binding d
252	23	100.0	86	5	ABP11210	Abp11210 Human ORF	325	23	100.0	107	7	ADD25816	Add25816 Binding d
253	23	100.0	86	6	ABM49077	Abm49077 Propionib	326	23	100.0	107	7	ADD25818	Add25818 Binding d
254	23	100.0	86	7	ADB32470	Adb32470 Human nov	327	23	100.0	107	7	ADD25817	Add25817 Binding d
255	23	100.0	87	4	AU17569	Au17569 Novel sig	328	23	100.0	107	7	ADD25661	Add25661 Binding d
256	23	100.0	87	4	AAM69444	Aam69444 Human imm	329	23	100.0	107	8	ADF89744	Adf89744 Human Clo
257	23	100.0	87	4	AAO9077	Aao9077 Human pol	330	23	100.0	107	8	ADH75386	Adh75386 Human Igg
258	23	100.0	87	4	AU43833	Au43833 Propionib	331	23	100.0	107	8	ADJ52133	Adj52133 CH1 delet
259	23	100.0	87	4	AU87465	Au87465 Novel cen	332	23	100.0	107	8	ADJ52130	Adj52130 CH1 delet
260	23	100.0	87	5	ABP64189	Abp64189 Human ORF	333	23	100.0	107	8	ADL90102	Adl90102 Human imm
261	23	100.0	87	5	ABM40352	Abm40352 Propionib	334	23	100.0	107	8	ADN36891	Adn36891 CH3 regio
262	23	100.0	87	7	ADB94277	Adb94277 Human nov	335	23	100.0	107	8	ADO60485	Ado60485 Humanised
263	23	100.0	87	8	ADI54780	Adi54780 Novel hum	336	23	100.0	107	8	ADS84435	Ads84435 Human ant
264	23	100.0	88	4	ABB36172	Abb36172 Peptide #	337	23	100.0	107	8	ADR68577	Adr68577 Human ant
265	23	100.0	88	4	AAM92663	Aam92663 Peptide #	338	23	100.0	108	3	AB42554	Ab42554 Human ORF
266	23	100.0	88	4	ABB21553	Abb21553 Protein #	339	23	100.0	108	4	AM21575	Am21575 Peptide #
267	23	100.0	88	4	ABG51016	Abg51016 Human liv	340	23	100.0	108	4	ABB43928	Abb43928 Peptide #
268	23	100.0	88	4	AAM04865	Aam04865 Peptide #	341	23	100.0	108	4	AM37854	Am37854 Peptide #
269	23	100.0	88	5	ABG38958	Abg38958 Human pep	342	23	100.0	108	4	ABB26843	Abb26843 Protein #
270	23	100.0	89	4	AAM92655	Aam92655 Human dig	343	23	100.0	108	4	AM77654	Am77654 Human bon
271	23	100.0	89	4	AAB60091	Aab60091 Human tra	344	23	100.0	108	4	AM64918	Am64918 Human bra
272	23	100.0	89	4	ABB16016	Abb16016 Human ner	345	23	100.0	108	4	ABG59302	Abg59302 Human liv
273	23	100.0	89	4	AAU22649	Aau22649 Novel hum	346	23	100.0	108	5	ABG46686	Abg46686 Human pep
274	23	100.0	89	7	ADB32489	Adb32489 Human nov	347	23	100.0	108	5	AAE28090	Aae28090 Human imm
275	23	100.0	89	7	ADJ68974	Adj68974 Human hea	348	23	100.0	109	4	AM89355	Am89355 Human imm
276	23	100.0	89	7	ADJ68975	Adj68975 Human hea	349	23	100.0	109	4	ABG01586	Abg01586 Novel hum
277	23	100.0	91	4	AAU60396	Aau60396 Propionib	350	23	100.0	110	4	AM62185	Am62185 Propionib
278	23	100.0	91	6	ABM56915	Abm56915 Propionib	351	23	100.0	110	4	AAU40774	Aau40774 Propionib
279	23	100.0	91	7	ADH76885	Adh76885 Mouse SOX	352	23	100.0	110	6	AM37293	Am37293 Propionib
280	23	100.0	92	3	AAB41836	Aab41836 Human COL	353	23	100.0	110	6	ABM58704	Abm58704 Propionib
281	23	100.0	92	4	AAG77595	Ag77595 Human col	354	23	100.0	110	8	ABO56225	Ab056225 Human gen
282	23	100.0	92	8	AM80295	Am80295 Tumour-as	355	23	100.0	110	8	ADR59167	Adr59167 Human Igg
283	23	100.0	94	4	AAU50673	Aau50673 Propionib	356	23	100.0	111	2	AAW13461	Aaw13461 Headpiece
284	23	100.0	94	4	ABG17384	Abg17384 Novel hum	357	23	100.0	111	4	AM88837	Am88837 Human imm
285	23	100.0	94	5	ABP41413	Abp41413 Human ova	358	23	100.0	111	4	AAO02130	Aao02130 Human pol
286	23	100.0	94	6	ABM47192	Abm47192 Propionib	359	23	100.0	111	8	ADM87720	Adm87720 Human EST
287	23	100.0	95	4	ABG28613	Abg28613 Novel hum	360	23	100.0	112	3	AAW13459	Aaw13459 Headpiece
288	23	100.0	95	5	ADK35495	Adk35495 Novel hum	361	23	100.0	112	3	AAW13070	Aaw13070 Pinus rad
289	23	100.0	95	7	ABO67894	Ab067894 Pseudomon	362	23	100.0	112	4	AAU43924	Aau43924 Propionib
290	23	100.0	96	4	AAO02842	Aao02842 Human pol	363	23	100.0	112	6	ABM40443	Abm40443 Propionib
291	23	100.0	96	6	ABO00435	Ab000435 Novel hum	364	23	100.0	112	8	ADR59166	Adr59166 Optimum C
292	23	100.0	96	6	ADB17005	Adb17005 Propionib	365	23	100.0	113	6	ABJ38539	Abj38539 Human son
293	23	100.0	98	4	AAU58604	Aau58604 Propionib	366	23	100.0	113	7	ABO63581	Ab063581 Klebssteli
294	23	100.0	98	4	ABG22290	Abg22290 Novel hum	367	23	100.0	113	8	ABO57697	Ab057697 Human gen
295	23	100.0	98	6	ABM55123	Abm55123 Propionib	368	23	100.0	114	4	AM38036	Am38036 Peptide #
296	23	100.0	99	4	AAU52200	Aau52200 Propionib	369	23	100.0	114	4	ABB26980	Abb26980 Protein #
297	23	100.0	99	6	ABM48719	Abm48719 Propionib	370	23	100.0	114	4	AM77817	Am77817 Human bon
298	23	100.0	100	4	ABM11942	Abm11942 Human dia	371	23	100.0	114	4	ABG59471	Abg59471 Human liv
299	23	100.0	100	4	AAW79957	Aaw79957 Human pro	372	23	100.0	114	5	ABG46848	Abg46848 Human pep
300	23	100.0	100	4	AAW93289	Aaw93289 Human pro	373	23	100.0	115	4	AAW74796	Aaw74796 Human col
301	23	100.0	100	8	ADF89743	Adf89743 Human Clo	374	23	100.0	115	6	ADA55196	Ada55196 Human pro
302	23	100.0	101	5	ABP08907	Abp08907 Human ORF	375	23	100.0	115	8	ADR09355	Adr09355 Human pro
303	23	100.0	102	3	AAW32715	Ag32715 Zee may	376	23	100.0	116	4	AAU49757	Aau49757 Propionib
304	23	100.0	102	4	AAU56849	Aau56849 Propionib	377	23	100.0	116	5	ABP07764	Abp07764 Human ORF
305	23	100.0	102	4	AAW99228	Aaw99228 Human pro	378	23	100.0	116	6	ABM46276	Abm46276 Propionib
306	23	100.0	102	5	ABM03349	Abm03349 Human ORF	379	23	100.0	117	2	AAW36147	Aaw36147 Rat eosin
307	23	100.0	102	6	ABM53368	Abm53368 Propionib	380	23	100.0	117	3	AAW44109	Aaw44109 Human can
308	23	100.0	102	7	ADB65769	Adb65769 Human pro	381	23	100.0	117	4	AM88573	Am88573 Human imm
309	23	100.0	104	2	AAW12501	Ag12501 Human 5'	382	23	100.0	117	4	AAO03150	Aao03150 Human pol
310	23	100.0	104	3	AAW12424	Ag12424 Zee may	383	23	100.0	118	3	AAW45071	Aaw45071 Human sec
311	23	100.0	105	4	AAW84107	Aaw84107 Human imm	384	23	100.0	118	4	AM78637	Am78637 Human pro
312	23	100.0	105	4	AAO00397	Aao00397 Human pol	385	23	100.0	118	4	AAO12123	Aao12123 Human pol
313	23	100.0	106	3	AAW32314	Aaw32314 Rice neut	386	23	100.0	118	4	ABG22738	Abg22738 Novel hum
314	23	100.0	107	2	AAW27681	Aar27681 Human imm	387	23	100.0	119	4	AM87975	Am87975 Human imm
315	23	100.0	107	2	AAW41718	AAW41718 Undefined	388	23	100.0	119	4	AAO03225	Aao03225 Human pol
316	23	100.0	107	2	AAW41685	AAW41685 Undefined	389	23	100.0	119	4	AAU42649	Aau42649 Propionib
317	23	100.0	107	2	AAW41714	AAW41714 Undefined	390	23	100.0	119	6	ABM39168	Abm39168 Propionib

391	23	100.0	120	3	AAG16111	Aag16111 Arabidops	464	23	100.0	136	6	ABP75637	Abp75637 Human sec
392	23	100.0	121	7	ADM04825	Adm04825 Human pro	465	23	100.0	136	8	ADG22372	Adg22372 Cyanophag
393	23	100.0	120	4	RAU65294	Rau65294 Propionib	466	23	100.0	137	3	RAG33352	Rag33352 Zea may
394	23	100.0	121	4	AAU61612	Aau61612 Propionib	467	23	100.0	137	3	AGG07099	Aag07099 Arabidops
395	23	100.0	121	6	ABM61813	Abm61813 Propionib	468	23	100.0	137	3	AGG47461	Aag47461 Arabidops
396	23	100.0	121	6	ABM58131	Abm58131 Propionib	469	23	100.0	138	3	AY70578	Aay70578 Salmonell
397	23	100.0	123	3	AAB53621	Aab53621 Human col	470	23	100.0	138	4	ABG25309	Abg25309 Novel hum
398	23	100.0	123	4	AAO00225	Aao00225 Human pol	471	23	100.0	139	4	AB42106	Ab42106 Human ORF
399	23	100.0	123	4	AAU41835	Aau41835 Propionib	472	23	100.0	139	5	ABP58510	Abp58510 Human mat
400	23	100.0	123	4	ABG00522	Abg00522 Novel hum	473	23	100.0	139	5	ABP58510	Abp58510 Human mat
401	23	100.0	123	6	ABM38354	Abm38354 Propionib	474	23	100.0	139	7	ADJ70416	Adj70416 Human hea
402	23	100.0	124	4	AAO04325	Aao04325 Human pol	475	23	100.0	140	4	AAO02927	Aao02927 Human pol
403	23	100.0	124	4	ABG02519	Abg02519 Novel hum	476	23	100.0	141	2	AY27815	Aay27815 Human sec
404	23	100.0	124	4	ABG16821	Abg16821 Novel hum	477	23	100.0	141	3	AAV32316	Aay32316 Soybean n
405	23	100.0	124	7	ADF60304	Adf60304 Human con	478	23	100.0	141	4	AAV32316	Aay32316 Soybean n
406	23	100.0	124	7	ADF06217	Adf06217 Bacterial	479	23	100.0	141	4	ABM18786	Abm18786 Peptide #
407	23	100.0	125	4	AAU41925	Aau41925 Propionib	480	23	100.0	141	4	ABM18786	Abm18786 Peptide #
408	23	100.0	125	6	ABM38444	Abm38444 Propionib	481	23	100.0	141	4	AAV32316	Aay32316 Soybean n
409	23	100.0	126	2	AAW97351	Aaw97351 Amino aci	482	23	100.0	141	4	ABM32145	Abm32145 Protein #
410	23	100.0	126	3	AAV32317	Aay32317 Wheat neu	483	23	100.0	141	4	AAW71016	Aam71016 Human bon
411	23	100.0	126	3	AAV32317	Aay32317 Wheat neu	484	23	100.0	141	4	AAW71016	Aam71016 Human bon
412	23	100.0	127	6	ADA57554	Ada57554 Human sec	485	23	100.0	141	4	ABG52731	Abg52731 Human liv
413	23	100.0	127	6	ADA41446	Ada41446 Human sec	486	23	100.0	141	4	ABG52731	Abg52731 Human liv
414	23	100.0	127	7	ADC74566	Adc74566 Human sec	487	23	100.0	141	5	ABG40807	Abg40807 Human pep
415	23	100.0	127	7	ADD38085	Add38085 Human sec	488	23	100.0	141	6	ABO14308	Abol14308 Novel hum
416	23	100.0	127	7	ADF94884	Adf94884 Human gen	489	23	100.0	141	7	ABO70522	Abol70522 Pseudomon
417	23	100.0	127	8	ADN41129	Adn41129 Novel hum	490	23	100.0	141	8	ADG78716	Adg78716 Human sec
418	23	100.0	128	2	AAO2690	Aao2690 Human sec	491	23	100.0	141	8	ADG78716	Adg78716 Human sec
419	23	100.0	128	4	AAO00602	Aao00602 Human pol	492	23	100.0	141	8	ABG58987	Abg58987 Human gen
420	23	100.0	128	4	AAU41509	Aau41509 Propionib	493	23	100.0	141	8	ADP29582	Adp29582 Human sec
421	23	100.0	128	6	ABM38028	Abm38028 Propionib	494	23	100.0	142	4	AAU47271	Aau47271 Propionib
422	23	100.0	128	7	ADA07369	Ada07369 Human sec	495	23	100.0	142	5	ABP00170	Abp00170 Human ORF
423	23	100.0	129	2	AAW78421	Aaw78421 Antibody	496	23	100.0	142	5	ABM43790	Abm43790 Propionib
424	23	100.0	129	4	AAO10803	Aao10803 Human pol	497	23	100.0	142	6	ABM46492	Abm46492 Propionib
425	23	100.0	129	5	ABU05841	Abu05841 M. tuberc	498	23	100.0	142	6	ABM46492	Abm46492 Propionib
426	23	100.0	129	5	ABR57965	Abbr57965 CH3 domai	499	23	100.0	143	5	ABP42507	Abp42507 Human ext
427	23	100.0	129	6	ABR55202	Abrr55202 Amino aci	500	23	100.0	143	7	ABO38358	Abob38358 Pseudomon
428	23	100.0	130	2	AAW78422	Aaw78422 Antibody	501	23	100.0	144	4	ABG03179	Abg03179 Novel hum
429	23	100.0	130	2	ABR10669	Abbr10669 Human pan	502	23	100.0	144	5	ABP00772	Abp00772 Human ORF
430	23	100.0	130	4	AAW92711	Aaw92711 Human dig	503	23	100.0	144	5	ABP00772	Abp00772 Human ORF
431	23	100.0	130	4	ABBI1212	Abbi1212 Human gro	504	23	100.0	144	7	ADF60370	Adf60370 Human con
432	23	100.0	130	4	AAU66197	Aau66197 Propionib	505	23	100.0	145	6	ABU08646	Abu08646 Cuphea ac
433	23	100.0	130	5	ABP04239	Abp04239 Human ORF	506	23	100.0	146	2	AAU59740	Aay59740 Human nor
434	23	100.0	130	5	ABR97978	Abbr97978 CH3 domai	507	23	100.0	146	5	ABR97978	Abbr97978 Human nor
435	23	100.0	130	6	ABM62716	Abm62716 Propionib	508	23	100.0	147	5	ABR97978	Abbr97978 Human pol
436	23	100.0	131	3	ABG16110	Aag16110 Arabidops	509	23	100.0	147	5	ABP63035	Abp63035 Human pol
437	23	100.0	131	4	AAO03385	Aao03385 Human pol	510	23	100.0	147	5	ABP63035	Abp63035 Human pol
438	23	100.0	131	8	ADF89745	Adf89745 Human Clo	511	23	100.0	148	4	AAU44948	Aau44948 Propionib
439	23	100.0	132	4	AAU64768	Aau64768 Propionib	512	23	100.0	148	4	AAU41354	Aau41354 Propionib
440	23	100.0	132	4	ABBI5735	Abbi5735 Human ner	513	23	100.0	148	4	AAU58749	Aau58749 Propionib
441	23	100.0	132	4	AAU20868	Aau20868 Human nov	514	23	100.0	148	4	ABG25700	Abg25700 Novel hum
442	23	100.0	132	6	ABM61287	Abm61287 Propionib	515	23	100.0	148	5	ABG25700	Abg25700 Novel hum
443	23	100.0	132	6	ABO00696	Abol00696 Novel hum	516	23	100.0	148	5	ABG25700	Abg25700 Novel hum
444	23	100.0	132	6	AAO16348	Aao16348 Zinc fing	517	23	100.0	148	6	ABM41467	Abm41467 Propionib
445	23	100.0	133	4	ABG19982	Abg19982 Novel hum	518	23	100.0	148	6	ABM37873	Abm37873 Propionib
446	23	100.0	133	7	ABO66675	Abol66675 Klebsiell	519	23	100.0	148	6	ABM55268	Abm55268 Propionib
447	23	100.0	133	8	ADN21278	Adn21278 Bacterial	520	23	100.0	148	7	ADH62347	Adh62347 Rhizomuco
448	23	100.0	134	3	ABR42969	Abrr42969 Human ORF	521	23	100.0	148	7	ABO72502	Abol72502 Pseudomon
449	23	100.0	134	3	ABR09067	Abrr09067 Hepatitis	522	23	100.0	149	3	ABG10091	Abg10091 Arabidops
450	23	100.0	134	4	ABM88513	Abm88513 Human imm	523	23	100.0	149	3	ABG10091	Abg10091 Arabidops
451	23	100.0	134	4	ABG03311	Abg03311 Novel hum	524	23	100.0	149	4	ABG14138	Abg14138 Novel hum
452	23	100.0	134	5	AAE21243	Aae21243 Human gen	525	23	100.0	149	4	ABG19445	Abg19445 Novel hum
453	23	100.0	134	5	ABR40510	Abrr40510 Human sec	526	23	100.0	149	4	ABG19445	Abg19445 Novel hum
454	23	100.0	134	5	ABR40432	Abrr40432 Human sec	527	23	100.0	149	6	ABM56777	Abm56777 Propionib
455	23	100.0	134	6	ABM65627	Abm65627 Propionib	528	23	100.0	149	6	ABM56777	Abm56777 Propionib
456	23	100.0	134	7	ADG77021	Adg77021 Human nuc	529	23	100.0	149	7	ABM59786	Abm59786 Connectiv
457	23	100.0	134	7	ABO78213	Abol78213 Pseudomon	530	23	100.0	150	4	ABG26030	Abg26030 Novel hum
458	23	100.0	134	7	ABO82543	Abol82543 Pseudomon	531	23	100.0	150	4	ABG26030	Abg26030 Novel hum
459	23	100.0	134	7	ABO75224	Abol75224 Pseudomon	532	23	100.0	152	2	AAV74030	Aay74030 Human pro
460	23	100.0	135	3	AAO10990	Aao10990 Arabidops	533	23	100.0	152	4	AAV74030	Aay74030 Human pro
461	23	100.0	135	4	ABM64066	Abm64066 Human pro	534	23	100.0	152	4	AAV74030	Aay74030 Human pro
462	23	100.0	135	7	ABR22649	Abrr22649 Zea may	535	23	100.0	152	4	ABM37133	Abm37133 Peptide #
463	23	100.0	136	3	AAG22649	Aag22649 Zea may	536	23	100.0	152	4	ABM37133	Abm37133 Peptide #

537	23	100.0	152	4	AAM70271	Aam70271 Human bon	610	23	100.0	166	3	AAV32311	Aay32311 Corn neut
538	23	100.0	152	4	AAM57851	Aam57851 Human bra	611	23	100.0	166	4	AAM18264	Aam18264 Peptide #
539	23	100.0	152	4	AAM05733	Aam05733 Peptide #	612	23	100.0	166	4	AAM15177	Aam15177 Peptide #
540	23	100.0	152	8	ABO58881	Abos8881 Human gen	613	23	100.0	166	4	ABs68346	Abbs68346 Drosophil
541	23	100.0	153	3	AB12146	Ab12146 Hydrophob	614	23	100.0	166	4	ABs34170	Abbs34170 Peptide #
542	23	100.0	153	4	AAM25859	Aam25859 Human pro	615	23	100.0	166	4	ABs37296	Abbs37296 Peptide #
543	23	100.0	153	6	ABU38866	Abu38866 Protein e	616	23	100.0	166	4	AAM27634	Aam27634 Peptide #
544	23	100.0	153	7	ABO78279	Ab078279 Pseudomon	617	23	100.0	166	4	AAM30756	Aam30756 Peptide #
545	23	100.0	154	4	ABs93197	Ab393197 Human pro	618	23	100.0	166	4	ABs29001	Abbs29001 Peptide #
546	23	100.0	154	7	ABO82559	Ab082559 Pseudomon	619	23	100.0	166	4	ABs32047	Abbs32047 Peptide #
547	23	100.0	154	7	ABO78086	Ab078086 Pseudomon	620	23	100.0	166	4	ABs22585	Abbs22585 Protein #
548	23	100.0	155	4	AU49773	Au49773 Propionib	621	23	100.0	166	4	AAM67343	Aam67343 Human bon
549	23	100.0	155	5	ABB80081	Abb80081 Human X-t	622	23	100.0	166	4	AAM70434	Aam70434 Human bon
550	23	100.0	155	5	AAM49002	Aam49002 Human X-t	623	23	100.0	166	4	AAO09591	Aao09591 Human pol
551	23	100.0	155	6	ABR44238	Ab44238 Human sec	624	23	100.0	166	4	AU42240	Au42240 Propionib
552	23	100.0	155	6	ABM46292	Abm46292 Propionib	625	23	100.0	166	4	AAM57998	Aam57998 Human bra
553	23	100.0	155	6	ABU63127	Abu63127 Human gro	626	23	100.0	166	4	ABG49006	Abg49006 Human liv
554	23	100.0	155	8	ADP81239	Adp81239 Protein o	627	23	100.0	166	4	ABG52114	Abg52114 Human liv
555	23	100.0	155	8	ADP81237	Adp81237 Protein o	628	23	100.0	166	4	AAM05878	Aam05878 Peptide #
556	23	100.0	156	3	AG32713	Aag32713 Zea mays	629	23	100.0	166	4	AAM02915	Aam02915 Peptide #
557	23	100.0	156	4	AU65539	Au65539 Propionib	630	23	100.0	166	4	ABG40068	Abg40068 Human pep
558	23	100.0	156	6	ABM62058	Abm62058 Propionib	631	23	100.0	166	5	ABG36981	Abg36981 Human pep
559	23	100.0	156	7	ABO82638	Ab082638 Pseudomon	632	23	100.0	166	6	ABM38759	Abm38759 Propionib
560	23	100.0	157	4	AU60019	Au60019 Propionib	633	23	100.0	166	7	ABO71493	Ab071493 Pseudomon
561	23	100.0	157	5	ABP73657	Abp73657 Candida a	634	23	100.0	167	3	ABs53263	Abbs53263 Human col
562	23	100.0	157	6	ABM56587	Abm56587 Propionib	635	23	100.0	167	8	ABO54950	Ab054950 Human gen
563	23	100.0	157	6	ABM56538	Abm56538 Propionib	636	23	100.0	168	4	AU30792	Au30792 Novel hum
564	23	100.0	158	4	AAM15625	Aam15625 Peptide #	637	23	100.0	168	6	ADA54175	Ada54175 Human pro
565	23	100.0	158	4	ABs34630	Abbs34630 Peptide #	638	23	100.0	168	6	ABs56758	Abbs56758 Human sec
566	23	100.0	158	4	AAM28123	Aam28123 Peptide #	639	23	100.0	169	7	ADE31068	Ade31068 Human dia
567	23	100.0	158	4	ABs29453	Abbs29453 Peptide #	640	23	100.0	169	7	ABO83162	Ab083162 Pseudomon
568	23	100.0	158	4	ABs20040	Abbs20040 Protein #	641	23	100.0	169	7	ABO72246	Ab072246 Pseudomon
569	23	100.0	158	4	AAM67816	Aam67816 Human bon	642	23	100.0	169	7	ABO76458	Ab076458 Pseudomon
570	23	100.0	158	4	AAM55420	Aam55420 Human bra	643	23	100.0	169	7	ABO77823	Ab077823 Pseudomon
571	23	100.0	158	4	ABG49453	Abg49453 Human liv	644	23	100.0	169	7	ABO74253	Ab074253 Pseudomon
572	23	100.0	158	4	AAM03368	Aam03368 Peptide #	645	23	100.0	169	7	ABO76000	Ab076000 Pseudomon
573	23	100.0	158	5	ABG37338	Abg37338 Human pep	646	23	100.0	170	2	AAR10685	Aar10685 TNF and 1
574	23	100.0	159	3	AG35191	Aag35191 Zea mays	647	23	100.0	170	7	ABO75068	Ab075068 Pseudomon
575	23	100.0	159	4	ABG20866	Abg20866 Novel hum	648	23	100.0	170	7	ABO72923	Ab072923 Pseudomon
576	23	100.0	159	6	ABU40159	Abu40159 Protein e	649	23	100.0	170	7	ABO60818	Ab060818 Klebsiell
577	23	100.0	159	7	ABO71251	Ab071251 Pseudomon	650	23	100.0	171	4	AU63745	Au63745 Propionib
578	23	100.0	160	3	AAV33941	Aay33941 A partial	651	23	100.0	171	4	ABG22251	Abg22251 Novel hum
579	23	100.0	160	3	ABA40913	Ab40913 Human ORF	652	23	100.0	171	6	ABM60264	Abm60264 Propionib
580	23	100.0	160	4	AU49924	Au49924 Propionib	653	23	100.0	171	7	ABO75885	Ab075885 Pseudomon
581	23	100.0	160	5	ABP05876	Abp05876 Human OR	654	23	100.0	171	8	ADG32615	Adg32615 Cyanophag
582	23	100.0	160	6	ABM46443	Abm46443 Propionib	655	23	100.0	172	4	AU23729	Au23729 Novel hum
583	23	100.0	160	8	ADS23556	Ad323556 Bacterial	656	23	100.0	172	4	AU18469	Au18469 Human end
584	23	100.0	161	8	ABO55412	Ab055412 Human gen	657	23	100.0	173	4	AU60428	Au60428 Propionib
585	23	100.0	162	3	ABs33055	Abbs33055 Pinus rad	658	23	100.0	173	6	ABM56947	Abm56947 Propionib
586	23	100.0	162	4	AAM39085	Aam39085 Human pol	659	23	100.0	173	8	ADN99372	Adn99372 Novel neu
587	23	100.0	162	4	AU55250	Au55250 Propionib	660	23	100.0	174	2	AAY20786	Aay20786 Human neu
588	23	100.0	162	4	AU51210	Au51210 Propionib	661	23	100.0	175	3	AAV44484	Aay44484 Human int
589	23	100.0	162	5	ABB89385	Abb89385 Human pol	662	23	100.0	177	4	AU25588	Au25588 Human G P
590	23	100.0	162	6	ABM47729	Abm47729 Propionib	663	23	100.0	177	8	ADG22280	Adg22280 Cyanophag
591	23	100.0	162	6	ABM56569	Abm56569 Propionib	664	23	100.0	178	4	AU47551	Au47551 Propionib
592	23	100.0	162	6	ABM62109	Abm62109 Propionib	665	23	100.0	178	6	ABM44070	Abm44070 Propionib
593	23	100.0	162	7	ADB63396	Adb63396 Human pro	666	23	100.0	178	7	ABO80234	Ab080234 Pseudomon
594	23	100.0	162	8	ADR08530	Adr08530 Human pro	667	23	100.0	179	4	ABG00072	Abg00072 Novel hum
595	23	100.0	163	2	AAY29213	Aay29213 Amino aci	668	23	100.0	179	7	ABO80126	Ab080126 Pseudomon
596	23	100.0	163	6	ABU41993	Abu41993 Protein e	669	23	100.0	180	2	AAV28235	Aay28235 Human int
597	23	100.0	164	4	AU67280	Au67280 Propionib	670	23	100.0	180	2	AAM85615	Aam85615 Human zcy
598	23	100.0	164	4	AAU57621	Aau57621 Propionib	671	23	100.0	180	2	AAY22197	Aay22197 Human EDI
599	23	100.0	164	6	ABM63799	Abm63799 Propionib	672	23	100.0	180	2	AAV41762	Aay41762 Human PRO
600	23	100.0	164	6	ABM54140	Abm54140 Propionib	673	23	100.0	180	2	AAM97350	Aam97350 Interleuk
601	23	100.0	165	2	AAV07481	Aay07481 Human pho	674	23	100.0	180	3	ABs33443	Abbs33443 Human PRO
602	23	100.0	165	3	AGI18779	Agi18779 Zea mays	675	23	100.0	180	3	AAV44459	Aay44459 Human int
603	23	100.0	165	3	AGG07098	Aag07098 Arabidops	676	23	100.0	180	3	ABs44318	Abbs44318 Human PRO
604	23	100.0	165	3	AGG33351	Aag33351 Zea mays	677	23	100.0	180	3	ABs18671	Abbs18671 Amino aci
605	23	100.0	165	3	AGG47460	Aag47460 Arabidops	678	23	100.0	180	3	ABs18755	Abbs18755 A human i
606	23	100.0	165	4	ABG01533	Abg01533 Novel hum	679	23	100.0	180	3	ABs15541	Abbs15541 Human imm
607	23	100.0	165	5	ABB80080	Abb80080 Human sec	680	23	100.0	180	3	AAV93973	Aay93973 Amino aci
608	23	100.0	165	5	AAM49001	Aam49001 Human X-t	681	23	100.0	180	3	ABO7686	Ab07686 A human i
609	23	100.0	165	8	ADP47087	Adp47087 Human pho	682	23	100.0	180	3	AAB07592	Aab07592 A human i

683	23	100.0	180	4	AAE10950	Rael10950 Human Zcy	756	23	100.0	180	7	ADA87026	Novel hum
684	23	100.0	180	4	AAU12394	Raul12394 Human PRO	757	23	100.0	180	7	ADA88129	Novel hum
685	23	100.0	180	4	AAU04950	Aau04950 Human PRO	758	23	100.0	180	7	ADA46517	Novel hum
686	23	100.0	180	4	AAB49894	Aab49894 Human PRO	759	23	100.0	180	7	ADA49766	Human int
687	23	100.0	180	4	AAG50920	Agb50920 Human PRO	760	23	100.0	180	7	ADB28547	Human PRO
688	23	100.0	180	4	AAG65242	Agb65242 Human cel	761	23	100.0	180	7	ADB29099	Human PRO
689	23	100.0	180	5	AAU99159	Aau99159 Human cho	762	23	100.0	180	7	ADA77051	Human PRO
690	23	100.0	180	6	ABB93361	Abb93361 AmIno aci	763	23	100.0	180	7	ADA26959	Human PRO
691	23	100.0	180	6	ABO17838	Abol17838 Novel hum	764	23	100.0	180	7	ADA88681	Novel hum
692	23	100.0	180	6	ABO25264	Abol25264 Novel hum	765	23	100.0	180	7	ADA97686	Human PRO
693	23	100.0	180	6	ABU81092	Abu81092 Human PRO	766	23	100.0	180	7	ADB27443	Human PRO
694	23	100.0	180	6	ABU72270	Abu72270 Novel hum	767	23	100.0	180	7	ADB22376	Novel hum
695	23	100.0	180	6	ABU66792	Abu66792 Human PRO	768	23	100.0	180	7	ADAg7067	Human PRO
696	23	100.0	180	6	ABU84950	Abu84950 Human sec	769	23	100.0	180	7	ADB22928	Human PRO
697	23	100.0	180	6	ABU59873	Abu59873 Novel sec	770	23	100.0	180	7	ADB23701	Human PRO
698	23	100.0	180	6	ABU61148	Abu61148 Human PRO	771	23	100.0	180	7	ADA92423	Novel hum
699	23	100.0	180	6	ABO25063	Abol25063 Human sec	772	23	100.0	180	7	ADB15486	Human PRO
700	23	100.0	180	6	ABU89697	Abu89697 Human int	773	23	100.0	180	7	ADB38738	Novel hum
701	23	100.0	180	6	ABU80417	Abu80417 Human sec	774	23	100.0	180	7	ADB38186	Novel hum
702	23	100.0	180	6	ABU67068	Abu67068 Human sec	775	23	100.0	180	7	ADB66658	Novel hum
703	23	100.0	180	6	ABG17974	Abg17974 Human ful	776	23	100.0	180	7	ADB31990	Human int
704	23	100.0	180	6	ABU72592	Abu72592 Human IL-	777	23	100.0	180	7	ADB89738	Human PRO
705	23	100.0	180	6	ADA45965	Ada45965 Novel hum	778	23	100.0	180	7	ADB90470	Human PRO
706	23	100.0	180	6	ADA76396	Ada76396 Human PRO	779	23	100.0	180	7	ADB39571	Novel hum
707	23	100.0	180	6	ADA19046	Ada19046 Human PRO	780	23	100.0	180	7	ADB73976	Human PRO
708	23	100.0	180	6	ADA43225	Ada43225 Human int	781	23	100.0	180	7	ADB47194	Novel hum
709	23	100.0	180	6	ADA61669	Ada61669 Homo sapi	782	23	100.0	180	7	ADB86801	Human PRO
710	23	100.0	180	6	ADB19454	Adb19454 Novel hum	783	23	100.0	180	7	ADB76692	Human PRO
711	23	100.0	180	6	ADB27995	Adb27995 Human PRO	784	23	100.0	180	7	ADB77406	Novel hum
712	23	100.0	180	6	ADA86474	Ada86474 Novel hum	785	23	100.0	180	7	ADB34563	Human PRO
713	23	100.0	180	6	ADB16038	Adb16038 Human PRO	786	23	100.0	180	7	ADB35667	Human PRO
714	23	100.0	180	6	ADA47824	Ada47824 Human PRO	787	23	100.0	180	7	ADB66893	Human PRO
715	23	100.0	180	6	ADA67619	Ada67619 Human PRO	788	23	100.0	180	7	ADB34011	Human PRO
716	23	100.0	180	6	ADB30626	Adb30626 Human PRO	789	23	100.0	180	7	ADB35115	Human PRO
717	23	100.0	180	6	ADA85922	Ada85922 Novel hum	790	23	100.0	180	7	ADB36219	Human PRO
718	23	100.0	180	6	ADA97134	Ada97134 Human PRO	791	23	100.0	180	7	ADB46614	Novel hum
719	23	100.0	180	6	ADA79438	Ada79438 Human PRO	792	23	100.0	180	7	ADC44118	Human sec
720	23	100.0	180	6	ADB87577	Adb87577 Novel hum	793	23	100.0	180	7	ADC61878	Human sec
721	23	100.0	180	6	ADB16779	Adb16779 Human PRO	794	23	100.0	180	7	ADC63842	Human sec
722	23	100.0	180	6	ADA91871	Ada91871 Novel hum	795	23	100.0	180	7	ADC66942	Human sec
723	23	100.0	180	6	ADB14934	Adb14934 Human PRO	796	23	100.0	180	7	ADC69066	Human sec
724	23	100.0	180	6	ADA25009	Ada25009 Novel hum	797	23	100.0	180	7	ADC63126	Human sec
725	23	100.0	180	6	ADB18895	Adb18895 Novel hum	798	23	100.0	180	7	ADC68191	Human sec
726	23	100.0	180	6	ADA94110	Ada94110 Human PRO	799	23	100.0	180	7	ADC41511	Human sec
727	23	100.0	180	6	ADB20006	Adb20006 Novel hum	800	23	100.0	180	7	ADC67566	Human sec
728	23	100.0	180	6	ADB13318	Adb13318 Human PRO	801	23	100.0	180	7	ADC62502	Human sec
729	23	100.0	180	6	ABO43371	Abol43371 Novel hum	802	23	100.0	180	7	ADC42135	Human sec
730	23	100.0	180	6	ABO19719	Abol19719 Novel hum	803	23	100.0	180	7	ADC50487	Novel hum
731	23	100.0	180	6	ADA12670	Ada12670 Human sec	804	23	100.0	180	7	ADC72034	Novel hum
732	23	100.0	180	6	ADA74572	Ada74572 Human PRO	805	23	100.0	180	7	ADC60013	Novel hum
733	23	100.0	180	6	ADB24805	Adb24805 Human PRO	806	23	100.0	180	7	ADC53020	Novel hum
734	23	100.0	180	6	ADA82329	Ada82329 Human PRO	807	23	100.0	180	7	ADC57374	Novel hum
735	23	100.0	180	6	ADA75292	Ada75292 Human PRO	808	23	100.0	180	7	ADC60565	Novel hum
736	23	100.0	180	6	ADA85370	Ada85370 Novel hum	809	23	100.0	180	7	ADC51040	Novel hum
737	23	100.0	180	6	ADA84818	Ada84818 Novel hum	810	23	100.0	180	7	ADC65567	Human PRO
738	23	100.0	180	6	ADB30074	Adb30074 Human PRO	811	23	100.0	180	7	ADC54665	Novel hum
739	23	100.0	180	6	ADA80602	Ada80602 Human PRO	812	23	100.0	180	7	ADC53626	Novel hum
740	23	100.0	180	6	ADA75844	Ada75844 Human PRO	813	23	100.0	180	7	ADC59149	Novel hum
741	23	100.0	180	6	ADA47069	Ada47069 Human PRO	814	23	100.0	180	7	ADC56027	Novel hum
742	23	100.0	180	6	ADB25365	Adb25365 Human PRO	815	23	100.0	180	7	ADC58597	Novel hum
743	23	100.0	180	6	ADA93541	Ada93541 Human PRO	816	23	100.0	180	7	ADD03271	Novel hum
744	23	100.0	180	6	ADB26891	Adb26891 Human PRO	817	23	100.0	180	7	ADC90263	Novel hum
745	23	100.0	180	6	ADB31178	Adb31178 Human PRO	818	23	100.0	180	7	ADC69682	Human PRO
746	23	100.0	180	6	ADA61106	Ada61106 Homo sapi	819	23	100.0	180	7	ADC48571	Human PRO
747	23	100.0	180	6	ADB24253	Adb24253 Human PRO	820	23	100.0	180	7	ADD10100	Human PRO
748	23	100.0	180	6	ADA96582	Ada96582 Human PRO	821	23	100.0	180	7	ADD04675	Novel hum
749	23	100.0	180	6	ADA81154	Ada81154 Human PRO	822	23	100.0	180	7	ADC80631	Novel hum
750	23	100.0	180	6	ADA96030	Ada96030 Human PRO	823	23	100.0	180	7	ADD11138	Human PRO
751	23	100.0	180	6	ADB26339	Adb26339 Human PRO	824	23	100.0	180	7	ADC48019	Human PRO
752	23	100.0	180	6	ADB21824	Adb21824 Novel hum	825	23	100.0	180	7	ADC80079	Novel hum
753	23	100.0	180	6	ABO19610	Abol19610 Novel hum	826	23	100.0	180	7	ADD09548	Human PRO
754	23	100.0	180	7	ADA77603	Ada77603 Human PRO	827	23	100.0	180	7	ADD41261	Novel hum
755	23	100.0	180	7	ADB18343	Adb18343 Human PRO	828	23	100.0	180	7	ADD52400	Human PRO

829	23	100.0	180	7	ADD53140	Human PRO	902	23	100.0	180	8	ADE89309	Human PRO
830	23	100.0	180	7	ADD53692	Novel hum	903	23	100.0	180	8	ADE18448	Human PRO
831	23	100.0	180	7	ADD51848	Human PRO	904	23	100.0	180	8	ADE88757	Human PRO
832	23	100.0	180	7	ADD02647	Human PRO	905	23	100.0	180	8	ADE89905	Human sec
833	23	100.0	180	7	ADD02081	Human PRO	906	23	100.0	180	8	ADF61545	Human sec
834	23	100.0	180	7	ADD54263	Novel hum	907	23	100.0	180	8	ADF40237	Human sec
835	23	100.0	180	7	ADE49504	Human sec	908	23	100.0	180	8	ADF46033	Human sec
836	23	100.0	180	7	ADD92580	Human PRO	909	23	100.0	180	8	ADE94777	Human PRO
837	23	100.0	180	7	ADD91476	Human PRO	910	23	100.0	180	8	ADE91188	Human PRO
838	23	100.0	180	7	ADE04090	Human PRO	911	23	100.0	180	8	ADE95329	Human PRO
839	23	100.0	180	7	ADE32387	Novel hum	912	23	100.0	180	8	ADE93439	Human PRO
840	23	100.0	180	7	ADE22319	Human PRO	913	23	100.0	180	8	ADF24429	Human sec
841	23	100.0	180	7	ADD79543	Human PRO	914	23	100.0	180	8	ADF40861	Human sec
842	23	100.0	180	7	ADE35558	Human sec	915	23	100.0	180	8	ADF23805	Human sec
843	23	100.0	180	7	ADE16672	Human sec	916	23	100.0	180	8	ADF33788	Human sec
844	23	100.0	180	7	ADD73287	Human sec	917	23	100.0	180	8	ADF35020	Human PRO
845	23	100.0	180	7	ADE42079	Human PRO	918	23	100.0	180	8	ADF27255	Human sec
846	23	100.0	180	7	ADE17896	Human PRO	919	23	100.0	180	8	ADF27891	Human sec
847	23	100.0	180	7	ADD92028	Human PRO	920	23	100.0	180	8	ADE92335	Novel hum
848	23	100.0	180	7	ADE33491	Novel hum	921	23	100.0	180	8	ADE90636	Human PRO
849	23	100.0	180	7	ADE34043	Novel hum	922	23	100.0	180	8	ADF41485	Human sec
850	23	100.0	180	7	ADD80095	Human PRO	923	23	100.0	180	8	ADF33164	Human sec
851	23	100.0	180	7	ADD93132	Human PRO	924	23	100.0	180	8	ADF25530	Human sec
852	23	100.0	180	7	ADD72645	Human sec	925	23	100.0	180	8	ADF26631	Human sec
853	23	100.0	180	7	ADE19552	Human PRO	926	23	100.0	180	8	ADF34420	Human sec
854	23	100.0	180	7	ADE19000	Human PRO	927	23	100.0	180	8	ADF46657	Human sec
855	23	100.0	180	7	ADE43196	Human PRO	928	23	100.0	180	8	ADE91783	Novel hum
856	23	100.0	180	7	ADD95985	Human PRO	929	23	100.0	180	8	ADG02362	Human PRO
857	23	100.0	180	7	ADE22871	Human PRO	930	23	100.0	180	8	ADG22148	Novel hum
858	23	100.0	180	7	ADD78989	Human PRO	931	23	100.0	180	8	ADG20218	Human PRO
859	23	100.0	180	7	ADE32939	Novel hum	932	23	100.0	180	8	ADF98124	Human PRO
860	23	100.0	180	7	ADE42631	Human PRO	933	23	100.0	180	8	ADG24341	Novel hum
861	23	100.0	180	7	ADE17296	Human sec	934	23	100.0	180	8	ADF98695	Human PRO
862	23	100.0	180	7	ADD80647	Human PRO	935	23	100.0	180	8	ADG03526	Human PRO
863	23	100.0	180	7	ADD89675	Human PRO	936	23	100.0	180	8	ADF99247	Human PRO
864	23	100.0	180	7	ADE40959	Human PRO	937	23	100.0	180	8	ADG16832	Human PRO
865	23	100.0	180	7	ADE04758	Human PRO	938	23	100.0	180	8	ADG05291	Human PRO
866	23	100.0	180	7	ABW02053	Human IL-	939	23	100.0	180	8	ADG19558	Human PRO
867	23	100.0	180	7	ADE92887	Human PRO	940	23	100.0	180	8	ADG13395	Human PRO
868	23	100.0	180	7	ADF47310	Human sec	941	23	100.0	180	8	ADG08452	Novel hum
869	23	100.0	180	7	ADG21596	Novel hum	942	23	100.0	180	8	ADG15622	Human PRO
870	23	100.0	180	7	ADG23237	Novel hum	943	23	100.0	180	8	ADF97020	Human PRO
871	23	100.0	180	7	ADF97572	Human PRO	944	23	100.0	180	8	ADG06205	Human PRO
872	23	100.0	180	7	ADG87377	Human PRO	945	23	100.0	180	8	ADG23789	Novel hum
873	23	100.0	180	7	ADG80636	Human PRO	946	23	100.0	180	8	ADG04078	Human PRO
874	23	100.0	180	7	ADG53067	Human sec	947	23	100.0	180	8	ADG24979	Novel hum
875	23	100.0	180	7	ADG60387	Human sec	948	23	100.0	180	8	ADG07276	Novel hum
876	23	100.0	180	7	ADG80084	Human PRO	949	23	100.0	180	8	ADG07828	Novel hum
877	23	100.0	180	7	ADH55376	Novel hum	950	23	100.0	180	8	ADG55323	Novel hum
878	23	100.0	180	7	ADH55928	Novel hum	951	23	100.0	180	8	ADG60987	Novel hum
879	23	100.0	180	7	ADI61147	Human sec	952	23	100.0	180	8	ADG62091	Novel hum
880	23	100.0	180	7	ADI64147	Novel hum	953	23	100.0	180	8	ADG82292	Human PRO
881	23	100.0	180	7	ADI65096	Novel hum	954	23	100.0	180	8	ADG57531	Novel hum
882	23	100.0	180	7	ADH82009	Novel hum	955	23	100.0	180	8	ADG56979	Novel hum
883	23	100.0	180	7	ADH81457	Novel hum	956	23	100.0	180	8	ADG55875	Novel hum
884	23	100.0	180	7	ADL16673	Human PRO	957	23	100.0	180	8	ADG58635	Novel hum
885	23	100.0	180	7	ADH82626	Novel hum	958	23	100.0	180	8	ADG71001	Novel hum
886	23	100.0	180	7	ADN16025	Novel hum	959	23	100.0	180	8	ADG58083	Novel hum
887	23	100.0	180	7	ADN16654	Novel hum	960	23	100.0	180	8	ADG53667	Novel hum
888	23	100.0	180	7	ADN15473	Novel hum	961	23	100.0	180	8	ADG71553	Novel hum
889	23	100.0	180	7	ADN14921	Novel hum	962	23	100.0	180	8	ADG50643	Human sec
890	23	100.0	180	7	ABO74034	Pseudomon	963	23	100.0	180	8	ADG81740	Human PRO
891	23	100.0	180	7	ADI63595	Novel hum	964	23	100.0	180	8	ADH30702	Human PRO
892	23	100.0	180	8	ADC81183	Novel hum	965	23	100.0	180	8	ADH12069	Novel hum
893	23	100.0	180	8	ADD76631	Human PRO	966	23	100.0	180	8	ADG50019	Human sec
894	23	100.0	180	8	ADD87995	Human PRO	967	23	100.0	180	8	ADG51891	Human sec
895	23	100.0	180	8	ADD86399	Human PRO	968	23	100.0	180	8	ADG52491	Novel hum
896	23	100.0	180	8	ADE75847	Human PRO	969	23	100.0	180	8	ADG54219	Novel hum
897	23	100.0	180	8	ADE48804	Human sec	970	23	100.0	180	8	ADG49395	Human sec
898	23	100.0	180	8	ADE23423	Human PRO	971	23	100.0	180	8	ADG81188	Human PRO
899	23	100.0	180	8	ADE23975	Human PRO	972	23	100.0	180	8	ADG56427	Novel hum
900	23	100.0	180	8	ADE24618	Human PRO	973	23	100.0	180	8	ADH12693	Novel hum
901	23	100.0	180	8	ADD87443	Human PRO	974	23	100.0	180	8	ADG48771	Human sec

975 23 100.0 180 8 ADG61539 Novel hum
976 23 100.0 180 8 ADH28626 Human PRO
977 23 100.0 180 8 ADG54771 Novel hum
978 23 100.0 180 8 ADG59811 Novel hum
979 23 100.0 180 8 ADG51267 Human sec
980 23 100.0 180 8 ADG59211 Human sec
981 23 100.0 180 8 ADG62667 Human PRO
982 23 100.0 180 8 ADI81235 Human PRO
983 23 100.0 180 8 ADH25692 Human neu
984 23 100.0 180 8 ADG09978 Novel hum
985 23 100.0 180 8 ADI15449 Novel hum
986 23 100.0 180 8 ADG09326 Novel hum
987 23 100.0 180 8 ADI14781 Novel hum
988 23 100.0 180 8 ADI18376 Novel hum
989 23 100.0 180 8 ADJ61725 Human int
990 23 100.0 180 8 ADL16634 Human PRO
991 23 100.0 180 8 ADL71294 Human IL-
992 23 100.0 180 8 ADJ63657 Novel hum
993 23 100.0 180 8 ADJ77552 Human PRO
994 23 100.0 180 8 ADJ65674 Human PRO
995 23 100.0 180 8 ADM27810 Human PRO
996 23 100.0 180 8 ADM17469 Human sec
997 23 100.0 180 8 ADL07303 Human sec
998 23 100.0 180 8 ADM42534 Human PRO
999 23 100.0 180 8 ADM28396 Human PRO
1000 23 100.0 180 8 ADL13792 Human int

ALIGNMENTS

RESULT 1
AAB07766
ID AAB07766 standard; peptide; 4 AA.
XX
AC AAB07766;
XX
AC
XX
DT 07-NOV-2000 (first entry)
XX
DE Peptide which is not present in arginine-proline peptides.
XX
KW Pro-inflammatory cytokine; interleukin; IL-6; IL-8; fibroblast;
KW keratinocyte; cosmetic; dermatological composition;
KW immunological dysfunction; skin; inflammation; aging; ultra-violet light.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "this residue is H-Thr"
FT FT
FT Misc-difference 4 /note= "this residue is Arg-OH"
FT FT
XX WO200043417-A1.
PN
XX
XX
XX 27-JUL-2000.
PD
XX
PF 06-JAN-2000; 2000WO-FR000031.
XX
XX 22-JAN-1999; 99FR-00000743.
XX
PA (SEDE-) SEDERMA.
XX
PI Lintrner K;
XX
XX WPI; 2000-505831/45.
XX
XX New arginine-proline peptides, useful in cosmetics and dermatology for
PT treating e.g. inflammation, inhibit overproduction of proinflammatory
PT interleukins.
XX
XX Claim 5; Page 10; 20pp; French.
PS
XX

CC The specification describes peptides which contain a proline and a
CC terminal arginine residue. The proviso is that the peptides are not
CC AAB07765-68 and AAB07801. The proviso is that the invention restore (and
CC reduce) the levels of the pro-inflammatory cytokines interleukin (IL)-6
CC and IL-8 to levels found in young tissue (fibroblasts and keratinocytes).
CC The peptides are useful in cosmetic and dermatological compositions for
CC prevention or treatment of immunological dysfunction of the skin, and
CC inflammation caused by physiological aging and normal exposure to ultra-
CC violet light
XX
SQ Sequence 4 AA;
Query Match 100.0%; Score 23; DB 3; Length 4;
Best Local Similarity 100.0%; Pred No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
Db 1 GQPR 4
RESULT 2
AAB92377
ID AAB92377 standard; peptide; 4 AA.
XX
AC AAB92377;
XX
DT 22-JUN-2001 (first entry)
XX
DE Miscellaneous peptide SEQ ID NO:1553.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US013576.
XX
XX 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
XX WPI; 2001-112059/12.
DR
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
XX Disclosure; Page 712; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases

CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention

XX Sequence 4 AA;
 SQ

Query Match 100.0%; Score 23; DB 4; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 1 GQPR 4

RESULT 3

ADJ81639
 ID ADJ81639 standard; peptide; 4 AA.

XX AC ADJ81639;

XX DT 06-MAY-2004 (first entry)

XX DE Dermatological composition #1.

XX KW dermatological; angiotensin converting enzyme inhibitor; cosmetic;
 KW topical use; hesperidin; angiotensin converting enzyme; facial skin.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 1 /note= "optionally modified with palmitoyl group"
 XX FT

XX PN WO2003068141-A2.

XX PD 21-AUG-2003.

XX PF 10-FEB-2003; 2003WO-FR000441.

XX PR 15-FEB-2002; 2002FR-00001967.

XX PA (SEDE-) SEDERMA.

XX PI Linthner K;

XX DR WPI; 2003-778888/73.

XX PT Cosmetic or dermatological compositions, useful for the treatment of bags
 PT under the eyes, comprise at least two of hesperidin or its derivatives,
 PT angiotensin converting enzyme (ACE)-inhibiting dipeptides and proline-
 PT arginine oligopeptides.

XX PS Claim 5; Page 23; 26pp; French.

XX CC The invention relates to novel cosmetic or dermatological compositions
 CC for topical use comprising at least two components selected from
 CC hesperidin or its derivatives, angiotensin converting enzyme (ACE)-
 CC inhibiting dipeptides and oligopeptides with a C-terminal prolyl-arginine
 CC motif. The compositions are useful for the treatment of facial skin,
 CC especially bags under the eyes, preferably by continuous topical delivery
 CC from particles, capsules, fabrics or clothing in direct contact with the
 CC skin or hair. This sequence represents an example of the compositions of
 CC the invention.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 23; DB 7; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||

Db 1 GQPR 4

RESULT 4

ADN03394
 ID ADN03394 standard; peptide; 4 AA.

XX AC ADN03394;

XX DT 17-JUN-2004 (first entry)

XX DE Exemplary peptide ligand for proteome analysis #120.

XX KW Peptide ligand; proteome; capture compound; mass spectrometry;

XX KW protein separation;
 KW matrix assisted laser desorption ionisation-time of flight; MALDI-TOF.

XX OS Unidentified.

XX PN US2003119021-A1.

XX PD 26-JUN-2003.

XX PF 16-JUL-2002; 2002US-00197954.

XX PR 16-JUL-2001; 2001US-0306019P.

XX PR 21-AUG-2001; 2001US-0314123P.

XX PR 11-MAR-2002; 2002US-0363433P.

XX PA (KOST/) KOSTER H.

XX PA (SIDD/) SIDDIQI S.

XX PA (LITT/) LITTLE D P.

XX PI Koster H, Siddiqi S, Little DP;

XX DR WPI; 2004-059185/06.

XX PT Collection of capture compounds capable of binding to biomolecules to
 PT form complexes that are stable under mass spectrometry conditions, useful
 PT for analysis of biomolecules, especially proteins.

XX PS Disclosure; SEQ ID NO 120; 165pp; English.

XX CC The invention relates to a collection of capture compounds capable of
 CC binding to biomolecules to form complexes that are stable under mass
 CC spectrometry conditions. The formulae for the capture compounds comprises
 CC sets of compounds of formula (I)-(III) given in the specification. Also
 CC included are analysis of biomolecules (by contacting a composition
 CC comprising a biomolecule with the above collection and identifying or
 CC detecting bound biomolecules), separating protein conformers (by
 CC contacting a composition comprising a biomolecule with the above
 CC collection, separating the members of the collection and identifying
 CC bound proteins), reducing diversity of a complex mixture of biomolecules
 CC (by contacting the mixture with the above collection and separating each
 CC set of complexes of capture compounds with biomolecules from the other
 CC sets) and identifying phenotype-specific biomolecules (by sorting cells
 CC from a single subject into sets according to a phenotype, contacting
 CC mixtures of biomolecules from each set with the above collection and
 CC comparing the patterns of biomolecule binding from each set). The
 CC collection of capture compounds is useful for the analysis of
 CC biomolecules, especially proteins (e.g. analysis of a proteome), using
 CC mass spectrometry, especially matrix assisted laser desorption ionisation
 CC time of flight (MALDI-TOF) mass spectrometry. The present sequence is an
 CC exemplary peptide ligand which may be incorporated into a capture
 CC compound of the invention.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 23; DB 8; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

```

Db      1 GQPR 4
|||||
1 GQPR 4

RESULT 5
ADQ93809
ID   ADQ93809 standard; peptide; 4 AA.
XX   AC   ADQ93809;
XX   DT   23-SEP-2004 (first entry)
XX   DE   Rigin-based tetrapeptide #1 used in topical and cosmetic composition.
XX   KW   Cosmetic; pharmaceutical; personal care; wrinkle; enlarged pore;
XX   KW   skin roughness; skin dryness; stretch mark; puffy eye; dark circle;
XX   KW   aging; textural discontinuity; crevice; bump; sagging; skin tightness;
XX   KW   discolourisation; blotching; sallowness; hyperpigmented skin region;
XX   KW   hyperkeratinisation; elastosis.
XX   OS   Synthetic.
XX   FH   Key   Location/Qualifiers
XX   FT   Modified-site 1 /note= "N-palmitoylated"
XX   FT   FT
XX   PN   US2004132667-A1.
XX   PD   08-JUL-2004.
XX   PF   10-DEC-2003; 2003US-00731921.
XX   PR   17-NOV-2003; 2003WO-EP014019.
XX   PA   (SEDE-) SEDERMA SAS.
XX   PI   Lintner K;
XX   PI   WPI; 2004-524913/50.
XX   DR
XX   PT   Topical composition useful for reducing visible signs of aging in human
XX   PT   skin such as fine lines, wrinkles, roughness, dryness, comprises specific
XX   PT   amount rigin-based tetrapeptide and specific tripeptide and additional
XX   PT   ingredient.
XX   PS   Claim 7; SEQ ID NO 3; 36pp; English.
XX   CC   The invention relates to pharmaceutical, personal care and cosmetic
XX   CC   compositions containing tripeptides and tetrapeptides. The composition
XX   CC   comprising additional ingredients rutin and Bowman Birk inhibitor and
XX   CC   dermatologically acceptable carrier is useful for reducing stretch marks,
XX   CC   compositions comprising additional ingredients berberine or chrysine and
XX   CC   a chelating agent and a dermatologically acceptable carrier is useful for
XX   CC   reducing dark circles under the eyes. The composition is useful for
XX   CC   reducing visible signs of aging in human skin such as fine lines,
XX   CC   wrinkles, enlarged pores, roughness, dryness, and other skin texture
XX   CC   defects such as stretch marks (caused by pregnancy, trauma or other
XX   CC   influences), bags under the eyes (puffy eyes) and dark circles. It is
XX   CC   useful for making cosmetics, personal care products, topical
XX   CC   pharmaceutical preparation or medicament for reducing visible signs of
XX   CC   aging. The compositions of the invention for reducing visible signs of
XX   CC   developmental of textural discontinuities, skin lines, crevices, bumps,
XX   CC   loss of skin elasticity, sagging, loss of skin firmness, loss of skin
XX   CC   tightness, loss of skin recoil from deformation, discolourisation,
XX   CC   blotching, sallowness, hyperpigmented skin regions, keratoses, abnormal
XX   CC   differentiation, hyperkeratinisation, elastosis, collagen breakdown,
XX   CC   stretch marks, dark circles, etc. The present sequence is a tetrapeptide
XX   CC   used in the composition of the invention.
XX   SQ   Sequence 4 AA;
Query Match      100.0%; Score 23; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Db      1 GQPR 4
|||||
1 GQPR 4

RESULT 6
ADQ03553
ID   ADQ03553 standard; peptide; 4 AA.
XX   AC   ADQ03553;
XX   DT   23-SEP-2004 (first entry)
XX   DE   Preferred tetrapeptide.
XX   KW   cosmetic composition; anti-aging; skin aging; wrinkle; skin elasticity;
XX   KW   itch.
XX   OS   Synthetic.
XX   FH   Key   Location/Qualifiers
XX   FT   Modified-site 1 /note= "Optionally N-palmitoylated"
XX   FT   FT
XX   PN   US2004120918-A1.
XX   PD   24-JUN-2004.
XX   PF   19-DEC-2003; 2003US-00742344.
XX   PR   12-MAY-2003; 2003FR-00005707.
XX   PA   (SEDE-) SEDERMA SAS.
XX   PI   Lintner K, Gabriele DE;
XX   PI   WPI; 2004-498814/47.
XX   DR
XX   PT   Cosmetic composition useful for preventing/treating wrinkles, comprising
XX   PT   polypeptide having anti-aging activity, ceramide providing improvement in
XX   PT   anti-aging activity of polypeptide, and additional ingredient.
XX   PS   Disclosure; SEQ ID NO 3; 34pp; English.
XX   CC   The invention relates to a cosmetic composition having anti-aging
XX   CC   activity. The cosmetic composition is useful for treating or preventing
XX   CC   the sign of skin aging in human. The cosmetic composition is useful in
XX   CC   cosmetics, personal care products, topical pharmaceutical preparations or
XX   CC   medicaments for reducing wrinkles. The cosmetic composition is useful for
XX   CC   therapeutically or prophylactically regulating a skin condition, which
XX   CC   includes delaying, minimising and/or preventing visible and/or tactile
XX   CC   discontinuities in skin e.g. texture irregularities in the skin. The
XX   CC   cosmetic composition is useful for improving skin appearance, preventing
XX   CC   and/or retarding the appearance of wrinkles, improving firmness and
XX   CC   elasticity of skin, softening and/or smoothening lips, hair and nails,
XX   CC   preventing and/or treating itch, diminishing wrinkles and fine lines by
XX   CC   repairing the skin tissue and the cutaneous barrier of the stratum
XX   CC   corneum. The cosmetic composition is used in shampoos, conditions, UV-
XX   CC   protecting products, styling gels, cleansers, etc. The cosmetic
XX   CC   composition is stable, safe, contains good aesthetics and
XX   CC   antiinflammatory agents, and does not contain consumer-unacceptable skin
XX   CC   irritants. The present sequence represents the amino acid sequence of a
XX   CC   preferred tetrapeptide used to illustrate the present invention.
XX   SQ   Sequence 4 AA;
Query Match      100.0%; Score 23; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 GQPR 4
|||||
1 GQPR 4

Query Match      100.0%; Score 23; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 GQPR 4
|||||
1 GQPR 4

```


Db 1 GQPR 4

RESULT 7
ADR42229 standard; peptide; 4 AA.
XX ADR42229;
AC
XX 21-OCT-2004 (first entry)
DT
XX Rigin related peptide ligand, SEQ ID 120.
DE
XX Human; ligand; Rigin.
KW
XX Homo sapiens.
OS
XX WO2004064972-A2.
FN
XX 05-AUG-2004.
PD
XX 16-JAN-2004; 2004WO-US001037.
PF
XX 16-JAN-2003; 2003US-0441398P.
PR
XX (HKPH-) HK PHARM INC.
PA
XX (KOE/) KOESTER H.
PA
XX Koester H, Little DP, Siddiqi SM, Grealish MP, Marappan S;
PI
XX Hassman CF, Yip P;
PI
XX WPI; 2004-642213/62.
DR
XX Identifying drug non-target biomolecules in mixture of biomolecules
PT
XX Involves interacting mixture of biomolecules with capture compounds
PT
XX Having high binding affinity and analyzing captured biomolecules to
PT
XX Identify drug non-targets.
PT
XX Disclosure; SEQ ID NO 120; 368pp; English.
PS
XX The present invention relates to a method for identifying drug non-target
CC
XX biomolecules in a mixture of biomolecules. The method comprises
CC
XX interacting mixture with capture compounds having moiety X which
CC
XX covalently binds to biomolecules with high affinity, moiety Y that
CC
XX increases selectivity of binding so that the capture compound binds to
CC
XX fewer biomolecules, and moiety Z for presenting X and Y, and analysing
CC
XX captured biomolecules to identify drug non-targets. The capture compound
CC
XX also optionally comprises a sorting function moiety Q and or a solubility
CC
XX function moiety W. The selectivity function moiety Y serves to modulate
CC
XX the reactivity function by reducing the number of groups to which the
CC
XX reactivity function moiety X bind, such as by steric hindrance and other
CC
XX interactions. Y is optionally a peptide ligand (ADR42112-ADR42256).
XX
SQ Sequence 4 AA;
Query Match 100.0%; Score 23; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 1 GQPR 4

RESULT 8
AAY02344 standard; peptide; 9 AA.
ID AAY02344
XX
AC AAY02344;
XX
XX 09-JUL-1999 (first entry)
DT
KW

Peptide used to screen EST databases to identify heparinase DNA sequence.

Heparanase; hp; modulator; heparin-binding growth factor;
cellular response; cytokine; cell interaction; plasma lipoprotein;
cellular susceptibility; infection; disintegration;
neurodegenerative plaque; wound healing; angiogenesis; restenosis;
atherosclerosis; inflammation; neurodegenerative disease; neutralise;
plasma heparin; micrometastasis; autoimmune lesion; renal failure.
XX
OS Synthetic.
XX
XX WO9911798-A1.
PN
XX 11-MAR-1999.
PD
XX 31-AUG-1998; 98WO-US017954.
PF
XX 02-SEP-1997; 97US-00922170.
PR
XX 02-JUL-1998; 98US-00109386.
PR
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA
XX (FRIE/) FRIEDMAN M M.
PA
XX Pecker I, Vlodavsky I, Feinstein E;
PI
XX WPI; 1999-302255/25.
PI
XX New human polynucleotide useful for treating angiogenesis, restenosis,
PT
XX and inflammation.
PT
XX Example 1; Page 25; 63pp; English.
PS
XX The specification describes a polypeptide having heparanase (hp)
CC
XX activity. The recombinant protein is used as a modulator of heparin-
CC
XX binding growth factors, cellular responses to heparin-binding growth
CC
XX factors and cytokines, cell interaction with plasma lipoproteins,
CC
XX cellular susceptibility to viral, protozoal and bacterial infections or
CC
XX disintegration of neurodegenerative plaques. Heparanase may be useful for
CC
XX conditions such as wound healing, angiogenesis, restenosis,
CC
XX atherosclerosis, inflammation, neurodegenerative diseases, and viral
CC
XX infections. Mammalian heparanase can be used to neutralize plasma
CC
XX heparin, and anti-heparanase antibodies may be applied for
CC
XX immunodetection and diagnosis of micrometastases, autoimmune lesions, and
CC
XX renal failure in biopsy specimens, plasma samples, and body fluids. The
CC
XX present sequence represents a sequence used in the course of the
CC
XX invention
CC
SQ Sequence 9 AA;
Query Match 100.0%; Score 23; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 6 GQPR 9

RESULT 9
AAB08848 standard; peptide; 9 AA.
ID AAB08848
XX
XX AAB08848;
AC
XX 15-JAN-2001 (first entry)
DT
XX Peptide found in protein encoded by ESTs related to heparanase cDNA.
DE
XX Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW
XX heparin-binding growth factor; cytokine; neurodegenerative plaque;
KW
XX wound healing; infection; burn; angiogenesis; restenosis;
KW
XX atherosclerosis; inflammation; neurodegenerative disease;

PT New antisense oligonucleotide hybridizable with a polynucleotide encoding
 PT a polypeptide with heparanase activity, useful for treating diseases such
 as cancer and autoimmune disorders.

PS Example 1; SEQ ID NO 8; 108pp; English.

XX The invention relates to an antisense oligonucleotide (ASO) comprising a
 CC polynucleotide or a polynucleotide analogue of at least 10 bases being
 CC hybridizable in vivo, under physiological conditions, with a portion of
 CC a polynucleotide strand encoding a polypeptide having heparanase
 CC catalytic activity. Also included are a method of in vivo downregulating
 CC heparanase activity (comprising administering the ASO in vivo), a method
 CC of treating a subject suffering from a pathological condition
 CC (characterised by heparanase activity, comprising administering ASO to
 CC the subject), a pharmaceutical composition comprising the ASO and a
 CC carrier, an antisense nucleic acid construct (comprising a promoter
 CC sequence and a polynucleotide sequence directing the synthesis of an
 CC antisense RNA sequence of at least 10 bases being hybridizable in vivo,
 CC under physiological conditions, with a polynucleotide strand encoding a
 CC polypeptide having heparanase catalytic activity), a method of in vivo
 CC downregulating heparanase activity (comprising administering in vivo the
 CC antisense nucleic acid construct), a pharmaceutical composition
 CC comprising the antisense nucleic acid construct and a carrier, and an
 CC antisense oligonucleotide comprising a polynucleotide or a polynucleotide
 CC analogue of at least 10 bases being hybridizable in vivo, under
 CC physiological conditions, with a portion of a polynucleotide strand being
 CC characterised by forming at least a portion of an untranslated region
 CC (UTR) for a polynucleotide strand encoding a polypeptide having
 CC heparanase catalytic activity. The methods and compositions of the
 CC present invention are useful for the prevention and/or treatment of
 CC diseases or conditions associated with aberrant heparanase activity, such
 CC as heparanase-dependent cancer, cancer, autoimmune reaction and
 CC inflammation. The present sequence is a human heparanase tryptic peptide
 CC used to design primers for cDNA isolation.

XX Sequence 9 AA;

SQ Query Match 100.0%; Score 23; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GQPR 4
 ||||
 Db 6 GQPR 9

RESULT 12
 ADM48714
 ID ADM48714 standard; protein; 9 AA.

XX ADM48714;

XX 03-JUN-2004 (first entry)

XX Human hpa protein tryptic peptide.

DE Transgenic animal; heparanase; cancer; viral infection; restenosis;
 KW neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;
 KW human.

XX Homo sapiens.

XX US2003217375-A1.

XX 20-NOV-2003.

XX 24-FEB-2003; 2003US-00371218.

XX 31-AUG-1998; 98WO-US017954.

PR 01-MAR-1999; 99US-00258892.

PR 06-FEB-2001; 2001US-00776874.

PR 19-NOV-2001; 2001US-00988113.

XX

PA (ZCHA/) ZCHARIA E.
 PA (VLOD/) VLODAVSKY I.
 PA (METZ/) METZGER S.
 PA (PECK/) PECKER I.
 PA (ILAN/) ILAN N.
 PA (CHAJ/) CHAJEK-SHAUL T.
 PA (GOLD/) GOLDSCHMIDT O.

XX Zcharia E, Vlodavsky I, Metzger S, Pecker I, Ilan N;
 PI Chajek-Shaul T, Goldschmidt O;

XX WPI; 2004-021918/02.

XX New transgenic non-human animal expressing heparinase, useful as models
 PT for human disease, such as cancers, viral infection, neurodegenerative
 PT diseases, restenosis, atherosclerosis and pulmonary disorders.

PS Example 1; SEQ ID NO 8; 106pp; English.

XX The present invention relates to a transgenic non-human animal whose
 CC genome comprises an exogenous polynucleotide sequence, including a
 CC promoter active in tissues of the non-human, a region encoding a human
 CC heparanase, where the promoter and the region encoding human heparanase
 CC are operably linked in the exogenous polynucleotide such that human
 CC heparanase is expressed in at least a portion of the cells of the non-
 CC human animal. The methods and compositions of the present invention are
 CC useful for the production of transgenic animals expressing heparanase, to
 CC be used as models for human diseases such as cancers, viral infection,
 CC restenosis, neurodegenerative diseases, atherosclerosis and pulmonary
 CC disorders. The present sequence is human hpa protein tryptic peptide used
 CC in the exemplification of the invention.

XX Sequence 9 AA;

SQ Query Match 100.0%; Score 23; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GQPR 4
 ||||
 Db 6 GQPR 9

RESULT 13

AAY34181

ID AAY34181 standard; peptide; 10 AA.

XX AAY34181;

XX 15-NOV-1999 (first entry)

XX Human pre-proheparanase protein sequence fragment #8.

XX Human; pre-proheparanase; platelet; wound healing; angiogenesis blocker;
 KW inflammation; psoriasis; diabetic retinopathy; solid tumour; arthritis;
 KW heparin degradation; anticoagulant neutralisation; asthma; CNS disease;
 KW inflammatory disease; vascular restenosis; atherosclerosis; diagnosis;
 KW tumour growth; fibroproliferative disorder; neurodegenerative disease;
 KW therapy.

XX Homo sapiens.

XX WO9943830-A2.

XX 02-SEP-1999.

XX 18-FEB-1999; 99WO-US001489.

XX 24-FEB-1998; 98US-0075706P.

PR 26-MAR-1998; 98US-0079401P.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Heinkrikson RL, Fairbanks MB, Mildner AM;
 XX WPI; 1999-540598/45.
 XX
 PT New isolated platelet heparanase polypeptides, used to develop products
 PT for, e.g. wound healing and blocking angiogenesis.
 XX
 PS Example 3; Fig 8; 57pp; English.
 XX
 CC This sequence represents a fragment of the human pre-proheparanase of the
 CC invention. The pre-proheparanase sequence was isolated from human
 CC platelets. The heparanase can be used for identifying agents which alter
 CC heparanase activity. The heparanase can be used for wound healing or for
 CC blocking angiogenesis or inflammation. It can be used for treating e.g.
 CC psoriasis, diabetic retinopathy or solid tumours, or for the degradation
 CC of heparin and the neutralisation of heparin's anticoagulant properties
 CC during surgery. Inhibitors of heparanase activity can be used in the
 CC treatment of arthritis, asthma, and other inflammatory diseases, vascular
 CC restenosis, atherosclerosis, tumour growth and progression.
 CC fibroproliferative disorders, and central nervous system (CNS) and
 CC neurodegenerative diseases. The products can also be used for detection
 CC and diagnosis. The purified heparanase, both recombinantly produced human
 CC heparanase and heparanase isolated from human platelet activity, allows
 CC for the convenient selection of compounds having anti-heparanase
 CC activity, i.e. inhibitors of heparanase activity, by measuring inhibition
 CC of heparanase activity. Inhibition of heparanase activity can be measured
 CC by blocking heparanase-mediated release of radioactive fragments from in
 CC vivo radiolabelled (HSPG)/heparin
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db |||||
 7 GQPR 10
 RESULT 14
 AAAY17071
 ID AAAY17071 standard; peptide; 10 AA.
 AC
 AC AAAY17071;
 XX
 DT 21-JUL-1999 (first entry)
 XX
 DE Human platelet heparanase peptide fragment 1.
 KW
 KW Heparanase; endoglucuronidase; heparan sulfate proteoglycan; enzyme;
 KW metastasis; angiogenesis; wound healing; angioplasty-induced restenosis;
 KW arteriosclerosis; atherosclerosis; inflammation; tissue development;
 KW human; HSPG.
 XX
 XX Homo sapiens.
 OS
 XX WO921975-A1.
 PN
 XX 06-MAY-1999.
 PD
 XX 28-OCT-1998; 98WO-AU000898.
 XX
 XX 28-OCT-1997; 97AU-00000062.
 PR
 PR 03-DEC-1997; 97AU-00000812.
 XX
 XX (AUS) UNIV AUSTRALIAN NAT.
 PA
 XX Freeman CG, Hulett MD, Parish CR, Hamdorf BJ;
 PI WPI; 1999-312956/26.
 XX
 XX Polynucleotides encoding mammalian endoglucuronidases, especially
 PT

PT heparanases, useful to promote wound healing.
 XX
 PS Claim 6; Page 58; 112pp; English.
 XX
 CC The invention relates to nucleic acid sequences that encode heparanase
 CC enzymes having endoglucuronidase activity. Recombinant heparanases are
 CC capable of removing the HS side chain from heparan sulfate proteoglycan
 CC (HSPG). Sulfated oligosaccharides, sulphonates or HSPG can be used to
 CC inhibit heparanase, this is useful for treatment of a physiological or
 CC medical condition associated with elevated heparanase activity, such as
 CC metastasis, angiogenesis, wound healing, angioplasty-induced restenosis,
 CC arteriosclerosis, atherosclerosis and inflammation. The human, murine and
 CC rat heparanases can be used to enhance wound healing, especially
 CC associated with tissue development and repair. The conditions mentioned
 CC above can be diagnosed using specific antibodies, and also using primers
 CC and probes specific for the heparanase polynucleotides. Other uses of the
 CC heparanases include sequencing sulfated molecules such as HSPG. Sequences
 CC AAAY17071-81 represent amino acid sequences of trypsin digest generated
 CC human platelet heparanase peptides
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db |||||
 7 GQPR 10
 RESULT 15
 AAP60496
 ID AAP60496 standard; protein; 11 AA.
 XX
 AC AAP60496;
 AC
 XX 25-MAR-2003 (revised)
 DT 28-JUL-1991 (first entry)
 XX
 DE Peptide with Fc receptor-blocking activity.
 XX
 KW Antiinflammatory; antiallergic; immunosuppressive.
 XX
 OS Synthetic.
 XX
 PN WO8601211-A.
 XX
 PD 27-FEB-1986.
 XX
 XX 10-AUG-1984; 84WO-EP000242.
 PF
 XX 10-AUG-1984; 84WO-BF000242.
 PR
 XX (MERE) MERCK PATENT GMBH.
 PA
 XX Hahn GS;
 PI
 XX WPI; 1986-068963/10.
 DR
 XX New active site peptide derivs. - blocking binding of immune complex or
 PT immunoglobulin to Fc receptors, useful e.g. for treating auto-immune
 PT disease.
 PT
 XX Claim 22; Page 78-79; 87pp; English.
 PS
 XX The sequence is an active-site compound which blocks immune- complex
 CC binding to Ig Fc receptors and/or Ig binding to lymphocyte Fc receptors.
 CC The peptide modulates immune complex-mediated immunosuppression,
 CC inflammation and tissue disruption, and reduces human allergic responses.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC
 XX Sequence 11 AA;
 SQ

Query Match 100.0%; Score 23; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|
|
|
|
DB 8 GQPR 11

RESULT 16

ABU03391
ID ABU03391 standard; protein; 11 AA.

XX AC ABU03391;

XX 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #171.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

XX WO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicx RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX Claim 10; SEQ ID NO 171; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 11 AA;

Query Match 100.0%; Score 23; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|
|
|
|
DB 8 GQPR 11

RESULT 17

ADD23535
ID ADD23535 standard; peptide; 11 AA.

XX AC ADD23535;

XX 15-JAN-2004 (first entry)

XX Breast cancer membrane protein (BCMP) peptide SEQ ID NO:271.

XX breast cancer; screening; diagnosis; breast cancer therapy;
KW breast cancer membrane protein; BCMP; cytostatic; vaccine; human.

XX Homo sapiens.

XX WO2003087831-A2.

XX 23-OCT-2003.

XX 10-APR-2003; 2003WO-GB001559.

XX 11-APR-2002; 2002GB-00008331.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Hudson LJ, Stamps AC, Terrett JA;

XX WPI; 2003-845381/78.

XX Screening, diagnosing and/or treating breast cancer by detecting a change
PT in expression or activity of a breast cancer membrane protein (BCMP)
PT polypeptide or encoding nucleic acid molecule.

XX Claim 1; SEQ ID NO 271; 81pp; English.

XX The present invention describes a method of screening for and/or
CC diagnosing breast cancer in a subject, and/or monitoring the
CC effectiveness of breast cancer therapy. The method comprises detecting
CC and/or quantifying in a biological sample obtained from the subject a
CC breast cancer membrane protein (BCMP) polypeptide and a nucleic acid
CC molecule. Also described: (1) an antibody, its functionally-active
CC fragment, derivative or analogue, that specifically binds to one or more
CC of the BCMP polypeptide; (2) a diagnostic kit comprising a capture
CC reagent specific for an BCMP polypeptide, reagents and instructions for
CC use; (3) a method for screening for anti-breast cancer agents that
CC interact with the BCMP polypeptide, comprising contacting the polypeptide
CC with a candidate agent, and determining whether or not the candidate
CC agent interacts with the polypeptide; (4) a method for screening for anti
CC -breast cancer agents that modulate the expression or activity of an BCMP
CC polypeptide or the nucleic acid molecule cited above, comprising
CC comparing the expression or activity of the polypeptide or nucleic acid
CC molecule, in the presence and absence of a candidate agent or in the
CC presence of a control agent, and determining whether the candidate agent
CC causes the expression or activity of the polypeptide or nucleic acid
CC molecule to change; and (5) an agent identified by the method of (3) or
CC (4), which interacts with the polypeptide or causes the expression or
CC activity of the polypeptide, or the expression of the nucleic acid
CC molecule to change. BCMPs have cytostatic activities, and can be used in
CC vaccines. The BCMP polypeptide, nucleic acid molecule, antibody, agent or
CC their derivatives, are useful in the manufacture of a medicament for the
CC treatment of breast cancer, where the composition is a vaccine. The
CC present sequence represents a BCMP peptide which is used in the
CC exemplification of the present invention.

```
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 23; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 8 GQPR 11

RESULT 18
AAU87007
ID AAU87007 standard; peptide; 12 AA.
XX
AC AAU87007;
XX
DT 21-MAY-2002 (first entry)
XX
DE Estradiol mimotope peptide #55.
XX
KW Estradiol; mimotope; estrone-3-glucuronide; steroid detection;
KW immunoassay; phage display; immunogen.
XX
OS Synthetic.
XX
PN WO200212270-A1.
XX
XX 14-FEB-2002.
XX
PD
XX
PF 26-JUL-2001; 2001WO-EP008705.
XX
PR 03-AUG-2000; 2000EP-00306613.
XX
XX (UNIL ) UNILEVER PLC.
PA (UNIL ) UNILEVER NV.
PA (UNIL ) HINDUSTAN LEVER LTD.
XX
XX Badley RA, Berry MJ, Williams SC;
XX
XX WPI; 2002-241729/29.
XX
XX Peptide mimotope capable of binding specifically to antibody specific to
XX estradiol, useful for assaying presence and/or amount of estradiol,
XX especially estrone-3-glucuronide in sample.
XX
XX Claim 3; Page 27; 57pp; English.
XX
XX The invention relates to a purified peptide mimotope capable of binding
XX specifically to an antibody specific to estradiol. Also included are a
XX solid support having immobilised (releasably or non-releasably) peptide
XX mimotopes, an immunoassay test device for the detection of estradiol in
XX the sample, comprising the mimotopes and an antibody capable of binding
XX specifically to the mimotopes to generate a detectable signal and an
XX isolated nucleic acid encoding the peptide mimotopes. The mimotope is
XX useful for assaying the presence and/or amount of estradiol preferably
XX estrone-3-glucuronide in a sample which is urine or serum sample to be
XX tested and is also utilised in an immunoassay test device, and further
XX can be used as immunogens. The mimotope be used to construct new, or
XX improve the performance of old, immunoassay test formats and devices.
XX They can, for example, be utilised essentially to tune the signal in
XX conventional displacement assays for the detection of estradiol. The
XX mimotope can be bound directly to certain assay surfaces which are
XX otherwise non-compatible with estradiol on such surfaces needing to be
XX bound to the surface by complexing with another - often proteinaceous -
XX molecule. The mimotope is capable of being bound to the antigen-binding
XX site of an antibody in a selective fashion in the presence of excess
XX quantities of other undesired materials, and tightly enough (i.e. with
XX high enough affinity) that when used in an immunoassay, it provides a
XX useful result). The present sequence is a peptide mimotopes of the
XX invention

SQ Sequence 12 AA;
Query Match 100.0%; Score 23; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 5 GQPR 8

RESULT 19
AAP51019
ID AAP51019 standard; protein; 13 AA.
XX
AC AAP51019;
XX
DT 25-MAR-2003 (revised)
DT 16-AUG-2002 (revised)
DT 06-SEP-1991 (first entry)
XX
XX Sequence encoded by the area around the linkage between Ch2 and Ch3 of hC
DE gamma 1.
XX
KW Hybrid immunoglobulin; mouse-human hybrid.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Region 1..6 /label= Ch2
FT Region 7..13 /label= Ch3
FT
XX
XX EP162319-A.
PN
XX
XX 27-NOV-1985.
PD
XX
XX 24-APR-1984; 84JP-00082432.
PF
XX
XX 24-APR-1984; 84JP-00082432.
PR
XX
XX (HONG/) HONJO T.
PA
XX
XX Honjo T;
PI
XX
XX WPI; 1985-297774/48.
DR
XX
XX N-PSDB; AAN50019.
XX
XX Intron free linking of genes of different origins - by inserting into
XX retrovirus then splicing in eucaryotic cell.
XX
XX Example; Fig 8d(ii); 30pp; English.
XX
XX The inventors claim a method for the intron free linking of genes of
XX different origins. The DNA sequence are esp. mouse and human
XX immunoglobulin genes; one coding for the variable region and the other
XX for the constant region. (Updated on 16-AUG-2002 to add missing OS
XX field.) (Updated on 25-MAR-2003 to correct PD field.)
XX
XX Sequence 13 AA;
Query Match 100.0%; Score 23; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 7 GQPR 10

RESULT 20
```

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ABU60996
ID ABU60996 standard; protein; 13 AA.
XX
AC ABU60996;
XX
DT 08-MAY-2003 (first entry)
XX
DE Lung specific protein (LSP) #99.
XX
KW Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis;
KW cancer monitoring; cancer staging; cancer imaging; lung cancer;
KW non-cancerous diseases of the lung; transgenic animal.
XX
OS Homo sapiens.
XX
PN WO200268633-A2.
XX
PD 06-SEP-2002.
XX
PF 21-NOV-2001; 2001WO-US043612.
XX
PR 22-NOV-2000; 2000US-0252500P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Recipon H, Chen S, Sun Y, Liu C;
XX
DR WPI; 2002-713376/77.
XX
PT New isolated human nucleic acid molecule and polypeptide, useful for
PT identifying, diagnosing, monitoring, staging, imaging and treating lung
PT cancer and non-cancerous diseases of the lung.
XX
PS Claim 11; Page 379; 389pp; English.
XX
CC The invention describes an isolated human nucleic acid (I) encoding any
CC of 120 10-1533 residue amino acid sequences (S1), given in the
CC specification, comprising any of 164 179-12421 base pair sequences (S2),
CC given in the specification. The methods and compositions of the present
CC invention are useful for identifying, diagnosing, monitoring, staging,
CC imaging and treating lung cancer and non-cancerous diseases of the lung.
CC They are also used for identifying lung tissue, monitoring and
CC identifying and/or designing antagonists of the polypeptide of the
CC invention, gene therapy, production of transgenic animals and production
CC of engineered lung tissue for treatment and research. This is the amino
CC acid sequence of a lung specific nucleic acid
XX
SQ Sequence 13 AA;
  Query Match 100.0%; Score 23; DB 5; Length 13;
  Best Local Similarity 100.0%; Pred. No. 3e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 3 GQPR 6

RESULT 21
ID AAM98739
XX
AC AAM98739 standard; peptide; 14 AA.
XX
AC AAM98739;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human peptide #2014 encoded by a SNP oligonucleotide.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
XX

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```

KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Disclosure; Page 4109; 4143pp; English.
XX
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms
XX
SQ Sequence 14 AA;
  Query Match 100.0%; Score 23; DB 4; Length 14;
  Best Local Similarity 100.0%; Pred. No. 3.2e+02;
  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 7 GQPR 10

RESULT 22
ID AAP82447
XX
AC AAP82447 standard; peptide; 15 AA.
XX
AC AAP82447;
XX
DT 10-MAR-2003 (revised)
DT 07-NOV-1990 (first entry)
XX
DE Immune-modulating oligopeptide.
XX
KW Immune system; Ig Fc receptors; rheumatoid arthritis; vasculitis;
KW autoimmune diseases; asthma; immunostimulant.
XX
OS Unidentified.
XX
PN US4752601-A.
XX

```

PD 21-JUN-1988.
 XX
 XX
 PF 01-APR-1986; 86US-00846930.
 XX
 XX 12-AUG-1983; 83US-00522739.
 PR
 XX (IMMU-) IMMUNETECH PHARM.
 PA
 XX Hahn GS;
 XX
 XX WPI; 1988-190340/27.
 DR
 XX Modulating immune complex-mediated immune response - by admin. of
 PT oligopeptide to block immune complex binding to immunoglobulin Fc
 PT receptors.
 PT
 XX Claim 1; Page 20; 20pp; English.
 PS
 XX This peptide is administered to mammals to modulate an immune-complex
 CC mediated response. It blocks immune-complex binding to Ig Fc receptors. It
 CC is administered in an amt. sufficient to modulate the proliferation or
 CC function of mononuclear cells or to reduce immune-complex mediated
 CC inflammation or tissue destruction. It is thus useful in the treatment of
 CC e.g. rheumatoid arthritis, glomerulonephritis, asthma, autoimmune
 CC diseases and anaemias. It is also an efficient immunostimulant. Residues
 CC 13-15 may be absent (one or a combination or all three). (Updated on 10-
 CC MAR-2003 to add missing OS field.)
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 100.0%; Score 23; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GQPR 4
 DB |||||
 7 GQPR 10
 RESULT 23
 AAY13277
 ID AAY13277 standard; peptide; 15 AA.
 XX
 AC AAY13277;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Naturally occurring variant of the glutenin epitope Y13221.
 XX
 KW Gluten; variant; gliadin; glutenin; gluten-sensitive T-cell; vaccine;
 KW gluten tolerance; gluten-sensitivity; celiac disease; CD; celiac sprue;
 KW tropical sprue; childhood food allergy; dermatitis herpetiformis; DH.
 XX
 OS Synthetic.
 XX
 PN EP905518-A1.
 XX
 PD 31-MAR-1999.
 XX
 PF 23-SEP-1997; 97EP-00202909.
 XX
 PR 23-SEP-1997; 97EP-00202909.
 XX
 PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 XX Koning F, Van De Wal Y, Drijfhout JW, Kooy-Winkelaar EMC;
 XX WPI; 1999-192792/17.
 XX
 XX New antigenic peptides of gluten and methods for isolating them, useful
 PT as diagnostic agents and for treatment of gluten sensitivity i.e. Celiac
 PT disease (CD).

XX Disclosure; Page 28; 58pp; English.
 PS
 XX Peptides AAY13220-13343 represents gluten derived peptides, and their
 CC variants. The specification describes a method to find and characterize
 CC peptides that are recognized by an intestinally derived gluten-sensitive
 CC T-cells. The method comprises establishing and contacting at least one
 CC gluten-sensitive T-cell clone with a mixture of gluten-derived peptides,
 CC and fractionating the mixture to select peptides that stimulate the
 CC clonal cells from bioactive fractions. Peptides AAY13220 (gliadin derived
 CC peptide) and AAY13221 (glutenin derived peptide) were identified using
 CC these methods, and can be used in pharmaceuticals/medicines (vaccines)
 CC for inducing tolerance to gluten, or to treat gluten-sensitivity, i.e.
 CC celiac disease (CD) or celiac sprue, tropical sprue, childhood food
 CC allergies and dermatitis herpetiformis (DH). The peptides are also useful
 CC for elimination of a group of gluten-sensitive T-cells, and for
 CC generating antibodies, T-cell receptors, anti-idiotypic B- or T-cells by
 CC immunization of a mammal with the peptide
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 100.0%; Score 23; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GQPR 4
 DB |||||
 1 GQPR 4
 RESULT 24
 AAY13300
 ID AAY13300 standard; peptide; 15 AA.
 XX
 AC AAY13300;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Naturally occurring variant of the glutenin epitope Y13221.
 XX
 KW Gluten; variant; gliadin; glutenin; gluten-sensitive T-cell; vaccine;
 KW gluten tolerance; gluten-sensitivity; celiac disease; CD; celiac sprue;
 KW tropical sprue; childhood food allergy; dermatitis herpetiformis; DH.
 XX
 OS Synthetic.
 XX
 PN EP905518-A1.
 XX
 PD 31-MAR-1999.
 XX
 PF 23-SEP-1997; 97EP-00202909.
 XX
 PR 23-SEP-1997; 97EP-00202909.
 XX
 PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
 PA (UYLE-) RIJKSUNIV LEIDEN.
 XX
 XX Koning F, Van De Wal Y, Drijfhout JW, Kooy-Winkelaar EMC;
 XX WPI; 1999-192792/17.
 XX
 XX New antigenic peptides of gluten and methods for isolating them, useful
 PT as diagnostic agents and for treatment of gluten sensitivity i.e. Celiac
 PT disease (CD).
 XX
 XX Disclosure; Page 35; 58pp; English.
 PS
 XX Peptides AAY13220-13343 represents gluten derived peptides, and their
 CC variants. The specification describes a method to find and characterize
 CC peptides that are recognized by an intestinally derived gluten-sensitive
 CC T-cells. The method comprises establishing and contacting at least one
 CC gluten-sensitive T-cell clone with a mixture of gluten-derived peptides,
 CC and fractionating the mixture to select peptides that stimulate the

CC clonal cells from bioactive fractions. Peptides AAY13220 (gliadin derived peptide) and AAY13221 (glutenin derived peptide) were identified using these methods, and can be used in pharmaceuticals/medicines (vaccines) for inducing tolerance to gluten, or to treat gluten-sensitivity, i.e. celiac disease (CD) or celiac sprue, tropical sprue, childhood food allergies and dermatitis herpetiformis (DH). The peptides are also useful for elimination of a group of gluten-sensitive T-cells, and for generating antibodies, T-cell receptors, anti-idiotypic B- or T-cells by immunization of a mammal with the peptide

XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 23; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
Db 1 GQPR 4

RESULT 25

AAV13251
ID AAY13251 standard; peptide; 15 AA.

XX AC AAY13251;

XX AC AAY13251;

DT 21-JUN-1999 (first entry)

XX Naturally occurring variant of the glutenin epitope Y13221.

DE Gluten; variant; gliadin; glutenin; gluten-sensitive T-cell; vaccine;

KW Gluten tolerance; gluten-sensitivity; celiac disease; CD; celiac sprue;

KM Tropical sprue; childhood food allergy; dermatitis herpetiformis; DH.

XX Synthetic.

OS EP905518-A1.

PN 31-MAR-1999.

XX 23-SEP-1997; 97EP-00202909.

XX 23-SEP-1997; 97EP-00202909.

XX (ZIEK-) ACAD ZIEKENHUIS LEIDEN.

PA (OYLE-) RIJKSUNIV LEIDEN.

XX Koning F, Van De Wal Y, Drijfhout JW, Kooy-Winkelaar EMC;

XX WPI; 1999-192792/17.

XX New antigenic peptides of gluten and methods for isolating them, useful as diagnostic agents and for treatment of gluten sensitivity i.e. Celiac disease (CD).

XX Disclosure; Page 21; 58pp; English.

XX Peptides AAY13220-13343 represents gluten derived peptides, and their variants. The specification describes a method to find and characterize peptides that are recognized by an intestinally derived gluten-sensitive T-cells. The method comprises establishing and contacting at least one gluten-sensitive T-cell clone with a mixture of gluten-derived peptides, and fractionating the mixture to select peptides that stimulate the clonal cells from bioactive fractions. Peptides AAY13220 (gliadin derived peptide) and AAY13221 (glutenin derived peptide) were identified using these methods, and can be used in pharmaceuticals/medicines (vaccines) for inducing tolerance to gluten, or to treat gluten-sensitivity, i.e. celiac disease (CD) or celiac sprue, tropical sprue, childhood food allergies and dermatitis herpetiformis (DH). The peptides are also useful for elimination of a group of gluten-sensitive T-cells, and for generating antibodies, T-cell receptors, anti-idiotypic B- or T-cells by immunization of a mammal with the peptide

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 23; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
Db 1 GQPR 4

RESULT 26

ADM08091
ID ADM08091 standard; peptide; 15 AA.

XX AC ADM08091;

XX 20-MAY-2004 (first entry)

XX Canine immunoglobulin group 2 lambda VL species framework 4 peptide 20.

DE canine; dog; heavy; immunoglobulin; antibody light chain variable domain;

KW antiallergic; allergy; IgG; gene therapy; group 2 lambda species;

KM VL framework; FR4.

XX Canis familiaris.

XX WO2003060080-A2.

XX 24-JUL-2003.

XX 20-DEC-2002; 2002WO-US041362.

XX 21-DEC-2001; 2001US-0344874P.

XX (IDEX-) IDEX LAB INC.

XX Krah ER, Guo H, Aiyappa A, Lawton R;

XX WPI; 2003-598521/56.

XX New canine heavy and light chain variable domain polypeptides, useful for treating canine allergy.

XX Claim 34; Page 102; 130pp; English.

XX The invention relates to a novel canine heavy or light chain variable domain polypeptide. The protein of the invention demonstrates CC antiallergic activity and may be useful for treating canine allergy, CC possibly via gene therapy. The current sequence is that of a canine CC immunoglobulin light chain variable domain framework (FR) peptide of the CC invention.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 23; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
Db 11 GQPR 14

RESULT 27

ADM07959
ID ADM07959 standard; peptide; 15 AA.

XX AC ADM07959;

XX 20-MAY-2004 (first entry)

XX

DE Canine immunoglobulin group 2 lambda VL genus framework 4 peptide 21.
 XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
 KW anti-allergic; allergy; IgE; gene therapy; group 2 lambda genus;
 KW VL framework; FR4.
 XX
 XX Canis familiaris.
 OS
 XX WO2003060080-A2.
 PN
 XX 24-JUL-2003.
 PD
 XX 20-DEC-2002; 2002WO-US041362.
 PF
 XX 21-DEC-2001; 2001US-0344874P.
 PR
 XX (IDEX-) IDEXX LAB INC.
 PA
 XX Krah ER, Guo H, Aiyappa A, Lawton R;
 PI WPI; 2003-598521/56.
 DR
 XX New canine heavy and light chain variable domain polypeptides, useful for
 XX treating canine allergy.
 PT
 XX Claim 33; Page 101; 130pp; English.
 PS
 XX The invention relates to a novel canine heavy or light chain variable
 CC domain polypeptide. The protein of the invention demonstrates
 CC anti-allergic activity and may be useful for treating canine allergy,
 CC possibly via gene therapy. The current sequence is that of a canine
 CC immunoglobulin light chain variable domain framework (FR) peptide of the
 CC invention.
 CC
 XX Sequence 15 AA;
 SQ

Query Match 100.0%; Score 23; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 11 GQPR 14

RESULT 28
 ABP55617
 ID ABP55617 standard; peptide; 16 AA.
 XX
 AC ABP55617;
 XX
 DT 20-FEB-2003 (first entry)
 XX
 DE Human cytokine peptide IL17beta.
 XX
 XX DPP10; dipeptidyl peptidase; prolyl oligopeptidase; enzyme; asthma;
 KW anti-inflammatory; antiasthmatic; antipsoriatic; antiarthritic;
 KW antirheumatic; vaccine; gene therapy; inflammatory disease;
 KW inflammatory bowel disease; atopy; rheumatoid arthritis; psoriasis;
 KW chromosome 2q14.
 XX
 XX Homo sapiens.
 OS
 XX WO200286113-A2.
 PN
 XX 31-OCT-2002.
 PD
 XX 24-APR-2002; 2002WO-GB001887.
 PF
 XX 24-APR-2001; 2001GB-00010044.
 PR 24-APR-2001; 2001GB-00010046.
 PR 12-OCT-2001; 2001GB-00024575.
 PR 12-OCT-2001; 2001GB-00024594.
 PR

XX (ISIS-) ISIS INNOVATIONS LTD.
 PA
 XX Cookson WOM, Moffat MF, Allen M, Lench N;
 PI
 XX WPI; 2003-093132/08.
 DR
 XX New nucleic acid sequence comprising DPP10 mRNA, useful for the
 XX manufacture of a medicament for regulating DPP10 protein expression or
 PT for preventing or treating inflammatory disease e.g., inflammatory bowel
 PT disease.
 PT
 XX Example 2; Fig 19; 321pp; English.
 PS
 XX The present invention describes a new isolated nucleic acid sequence (I)
 CC comprising a DPP10 mRNA sequence. DPP10 is a dipeptidyl peptidase (also
 CC known as prolyl oligopeptidase). (I) has anti-inflammatory, antiasthmatic,
 CC antipsoriatic, antiarthritic and antirheumatic activities, and can be
 CC used in vaccines and gene therapy. A composition comprising (I) can be
 CC used for the manufacture of a medicament for regulating DPP10 expression
 CC or for preventing or treating inflammatory disease e.g., inflammatory
 CC bowel disease, asthma, atopy, rheumatoid arthritis or psoriasis. (I) can
 CC also be used in an assay for detecting or measuring DPP10 in a sample. A
 CC host cell comprising (I) can be used for producing recombinant DPP10 gene
 CC products, or in drug screening systems to identify agents for diagnosis
 CC or treatment of individuals having or susceptible to inflammatory
 CC disease. Human DPP10 is located on chromosome 2, more specifically
 CC chromosome 2q14. ABQ84254 to ABQ84612 and ABP55569 to ABP55629 represent
 CC sequences used in the exemplification of the present invention
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 23; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 6 GQPR 9

RESULT 29
 AAB36861
 ID AAB36861 standard; peptide; 17 AA.
 XX
 AC AAB36861;
 XX
 DT 20-FEB-2001 (first entry)
 XX
 DE Residues 334 to 351 of IgG.
 XX
 KW IgG; complement pathway; autoimmune.
 XX
 OS Unidentified.
 OS
 XX WO200064327-A2.
 PN
 XX 02-NOV-2000.
 PD
 XX 25-APR-2000; 2000WO-US010928.
 PF
 XX 26-APR-1999; 99US-0130936P.
 PR
 XX (UYDU-) UNIV DUKE.
 PA
 XX Frank MM, Jiang HJ;
 PI
 XX WPI; 2000-687249/67.
 DR
 XX Blocking complement pathway, useful for preventing immunologic damage in
 PT diseases such as autoimmune disease or in hyperacute xenograft rejection,
 PT by the administration of a complement pathway blocking peptide.
 XX

PS Claim 3; Page 16; 20pp; English.

CC The present invention relates to complement pathway blocking peptide

CC fragment. The peptide is used to treat a patient suffering from

CC autoimmune disease by blocking the complement pathway, thus preventing

CC immunologic tissue damage, or to treat a patient who is a recipient of a

CC xenograft. The peptide blocks the complement pathway without any tissue

CC damage and disease i.e., without subjecting the patient to an

CC unacceptable risk of the infection

XX Sequence 17 AA;

SQ

Query Match 100.0%; Score 23; DB 3; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db ||||

8 GQPR 11

RESULT 30

AAR49648

ID AAR49648 standard; peptide; 18 AA.

XX AAR49648;

AC

XX 25-MAR-2003 (revised)

DT 22-AUG-1994 (first entry)

XX

Sequence of peptide for domain 3 of the constant (C) region of the heavy

DE (H) chain (CH3) of an immunoglobulin (Ig).

DE

XX Immunoglobulin; heavy chain; constant region; Camelid.

KW

XX Camelus dromedarius.

OS

XX WO9404678-A1.

PN

XX 03-MAR-1994.

PD

XX 18-AUG-1993; 93WO-EP002214.

PF

XX 21-AUG-1992; 92EP-00402326.

PR

XX 21-MAY-1993; 93EP-00401310.

PR

XX (CAST/) CASTERMAN C.

PA (HAME/) HAMERS R.

PA

XX Casterman C, Hamers R;

PI

XX WPI; 1994-083195/10.

DR

XX Immunoglobulins devoid of light chains - also processes for their

PT preparation, and protein and nucleotide sequence encoding them.

PT

XX Claim 10; Page 61; 87pp; English.

PS

XX A novel immunoglobulin (Ig) is claimed which comprises two heavy (H)

CC polypeptide chains sufficient for the formation of a complete antigen

CC binding site or several such chains. The Ig is devoid of light (L)

CC polypeptide chains. The Ig may be obt. from prokaryotic cells, esp. E.

CC coli, by; cloning a DNA or cDNA sequence coding for the VH domain of an

CC Ig devoid of L chains obtainable from e.g. lymphocytes of Camelids;

CC recovering the cloned fragment after amplification using a 5' primer

CC contg. an Xho site and a 3' primer contg. the Spe site having the

CC sequence in AA04383; cloning the recovered fragment is a vector;

CC transforming host cells; and recovering the expression product of the VHH

CC coding sequence. A claimed Ig comprises 4 frameworks in its variable (V)

CC region selected from: sequences in AAR49611-16 and AAR49720 for the

CC framework 1 domain; AAR49617-21 for the framework 4 domain; and/or

CC AAR49622-39 for the CDR3 domain; and/or that its constant region

CC comprises CH2 and CH3 domains comprising AA sequences selected from, for

CC the CH2 domain AAR49640-3, and for the CH3 domain AAR49444-48; and/or that

CC its hinge region comprises 0-50 AAs, esp. a sequence selected from

CC AAR49649 or AAR49650. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 18 AA;

SQ

CC the CH2 domain AAR49640-3, and for the CH3 domain AAR49444-48; and/or that

CC its hinge region comprises 0-50 AAs, esp. a sequence selected from

CC AAR49649 or AAR49650. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 18 AA;

SQ

Query Match 100.0%; Score 23; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db ||||

1 GQPR 4

RESULT 31

AAR49647

ID AAR49647 standard; peptide; 18 AA.

XX AAR49647;

AC

XX 25-MAR-2003 (revised)

DT 22-AUG-1994 (first entry)

XX

Sequence of peptide for domain 3 of the constant (C) region of the heavy

DE (H) chain (CH3) of an immunoglobulin (Ig).

DE

XX Immunoglobulin; heavy chain; constant region; Camelid.

KW

XX Camelus dromedarius.

OS

XX WO9404678-A1.

PN

XX 03-MAR-1994.

PD

XX 18-AUG-1993; 93WO-EP002214.

PF

XX 21-AUG-1992; 92EP-00402326.

PR

XX 21-MAY-1993; 93EP-00401310.

PR

XX (CAST/) CASTERMAN C.

PA (HAME/) HAMERS R.

PA

XX Casterman C, Hamers R;

PI

XX WPI; 1994-083195/10.

DR

XX Immunoglobulins devoid of light chains - also processes for their

PT preparation, and protein and nucleotide sequence encoding them.

PT

XX Claim 10; Page 61; 87pp; English.

PS

XX A novel immunoglobulin (Ig) is claimed which comprises two heavy (H)

CC polypeptide chains sufficient for the formation of a complete antigen

CC binding site or several such chains. The Ig is devoid of light (L)

CC polypeptide chains. The Ig may be obt. from prokaryotic cells, esp. E.

CC coli, by; cloning a DNA or cDNA sequence coding for the VH domain of an

CC Ig devoid of L chains obtainable from e.g. lymphocytes of Camelids;

CC recovering the cloned fragment after amplification using a 5' primer

CC contg. an Xho site and a 3' primer contg. the Spe site having the

CC sequence in AA04383; cloning the recovered fragment is a vector;

CC transforming host cells; and recovering the expression product of the VHH

CC coding sequence. A claimed Ig comprises 4 frameworks in its variable (V)

CC region selected from: sequences in AAR49611-16 and AAR49720 for the

CC framework 1 domain; AAR49617-21 for the framework 4 domain; and/or

CC AAR49622-39 for the CDR3 domain; and/or that its constant region

CC comprises CH2 and CH3 domains comprising AA sequences selected from, for

CC the CH2 domain AAR49640-3, and for the CH3 domain AAR49444-48; and/or that

CC its hinge region comprises 0-50 AAs, esp. a sequence selected from

CC AAR49649 or AAR49650. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 18 AA;

SQ

```

Query Match      100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      1 GQPR 4

RESULT 32
AAR49646
ID AAR49646 standard; peptide; 18 AA.
XX AC AAR49646;
XX DT 25-MAR-2003 (revised)
DT 22-AUG-1994 (first entry)
XX DE Sequence of peptide for domain 3 of the constant (C) region of the heavy
DE (H) chain (CH3) of an immunoglobulin (Ig).
XX KW Immunoglobulin; heavy chain; constant region; Camelid.
XX OS Camelus dromedarius.
XX PN WO9404678-A1.
XX PD 03-MAR-1994.
XX PF 18-AUG-1993; 93WO-EP002214.
XX PR 21-AUG-1992; 92EP-00402326.
XX PR 21-MAY-1993; 93EP-00401310.
XX PA (CAST/) CASTERMAN C.
PA (HAME/) HAMERS R.
XX PI Casterman C, Hamers R;
XX WPI; 1994-083195/10.
XX
XX Immunoglobulins devoid of light chains - also processes for their
XX preparation, and protein and nucleotide sequence encoding them.
XX Claim 10; Page 61; 87pp; English.
XX
XX A novel immunoglobulin (Ig) is claimed which comprises two heavy (H)
XX polypeptide chains sufficient for the formation of a complete antigen
XX binding site or several such chains. The Ig is devoid of light (L)
XX polypeptide chains. The Ig may be obtd. from prokaryotic cells, esp. E.
XX coli, by: cloning a DNA or cDNA sequence coding for the VH domain of an
XX Ig devoid of L chains obtainable from e.g. lymphocytes of Camelids;
XX recovering the cloned fragment after amplification using a 5' primer
XX contg. an Xho site and a 3' primer contg. the Spe site having the
XX sequence in AA04383; cloning the recovered fragment is a vector;
XX transforming host cells; and recovering the expression product of the VH
XX coding sequence. A claimed Ig comprises 4 frameworks in its variable (V)
XX region selected from: sequences in AAR49611-16 and AAR49720 for the
XX framework 1 domain; AAR49617-21 for the framework 4 domain; and/or
XX AAR49622-39 for the CDR3 domain; and/or that its constant region
XX comprises CH2 and CH3 domains comprising AA sequences selected from, for
XX the CH2 domain AAR49640-3, and for the CH3 domain AAR49444-48, and/or that
XX its hinge region comprises 0-50 AAs, esp. a sequence selected from
XX AAR49649 or AAR49650. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 AA;

Query Match      100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      1 GQPR 4

RESULT 33
AAR49534
ID AAR49534 standard; peptide; 18 AA.
XX AC AAR49534;
XX DT 25-MAR-2003 (revised)
DT 04-SEP-1994 (first entry)
XX DE Human Ig heavy chain constant region CH3 gamma-4.
XX KW Immunoglobulin; Ig; heavy chain; constant region; antibody engineering;
KW IgG2; IgG3.
XX OS Homo sapiens.
XX PN EP584421-A1.
XX PD 02-MAR-1994.
XX PF 21-AUG-1992; 92EP-00402326.
XX PR 21-AUG-1992; 92EP-00402326.
XX PA (CAST/) CASTERMAN C.
PA (HAME/) HAMERS R.
XX PI Casterman C, Hamers R;
XX WPI; 1994-067061/09.
XX
XX New isolated immunoglobulin molecules devoid of light polypeptide chains
XX - consisting of heavy polypeptide chains only, obtd. from Camelid serum,
XX for use as antibodies.
XX Disclosure; Page 22; 35pp; English.
XX
XX This Ig heavy chain constant region CH3 gamma-4 sequence corresponds to
XX the equivalent gamma-3 sequence (AAR49531) of a camel 2-chain Ig molecule
XX (100 kDa) which lacks any light chains. The Ig has e.g. improved
XX solubility and aggregate much less than heavy chains of 4-chain Igs. The
XX Igs can be used normally for e.g. diagnosis, therapy, in vaccines, for
XX isolation and purification of antigens and in the production of anti-
XX idiotypic antibodies. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 AA;

Query Match      100.0%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GQPR 4
      ||||
Db      1 GQPR 4

RESULT 34
AAR49533
ID AAR49533 standard; peptide; 18 AA.
XX AC AAR49533;
XX DT 25-MAR-2003 (revised)
DT 04-SEP-1994 (first entry)
XX DE Human Ig heavy chain constant region CH3 gamma-2/gamma-3.
XX KW Immunoglobulin; Ig; heavy chain; constant region; antibody engineering;
KW IgG2; IgG3.
XX

```

OS Homo sapiens.
 XX EP584421-A1.
 XX
 XX PD 02-MAR-1994.
 XX
 XX PF 21-AUG-1992; 92EP-00402326.
 XX
 XX PR 21-AUG-1992; 92EP-00402326.
 XX
 XX PA (CAST/) CASTERMAN C.
 XX (HAME/) HAMERS R.
 XX
 XX PI Casterman C, Hamers R;
 XX WPI; 1994-067061/09.
 XX
 XX PT New isolated immunoglobulin molecules devoid of light polypeptide chains
 PT - consisting of heavy polypeptide chains only, obt'd. from Camelid serum,
 PT for use as antibodies.
 XX
 XX PS Disclosure; Page 22; 35pp; English.
 XX
 XX CC This Ig heavy chain constant region CH3 gamma-2/gamma-3 sequence
 CC corresponds to the equivalent gamma-3 sequence (AAR49531) of a camel 2-
 CC chain Ig molecule (100 kDa) which lacks any light chains. The Ig has e.g.
 CC improved solubility and aggregate much less than heavy chains of 4-chain
 CC IgG. The IgG can be used normally for e.g. diagnosis, therapy, in
 CC vaccines, for isolation and purification of antigens and in the
 CC production of anti-idiotypic antibodies. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 XX SQ Sequence 18 AA;
 XX
 XX Query Match 100.0%; Score 23; DB 2; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 GQPR 4
 XX ||||
 XX 1 GQPR 4
 XX
 XX RESULT 35
 XX AAR49532
 XX ID AAR49532 standard; peptide; 18 AA.
 XX
 XX AC AAR49532;
 XX
 XX DT 25-MAR-2003 (revised)
 XX 04-SEP-1994 (first entry)
 XX
 XX DE Human Ig heavy chain constant region CH3 gamma-1.
 XX
 XX KW Immunoglobulin; Ig; heavy chain; constant region; antibody engineering;
 XX IgG2; IgG3.
 XX
 XX OS Homo sapiens.
 XX
 XX XX EP584421-A1.
 XX
 XX PD 02-MAR-1994.
 XX
 XX PF 21-AUG-1992; 92EP-00402326.
 XX
 XX PR 21-AUG-1992; 92EP-00402326.
 XX
 XX PA (CAST/) CASTERMAN C.
 XX (HAME/) HAMERS R.
 XX
 XX PI Casterman C, Hamers R;
 XX WPI; 1994-067061/09.
 XX

XX New isolated immunoglobulin molecules devoid of light polypeptide chains
 PT - consisting of heavy polypeptide chains only, obt'd. from Camelid serum,
 PT for use as antibodies.
 XX
 XX PS Disclosure; Page 22; 35pp; English.
 XX
 XX CC This Ig heavy chain constant region CH3 gamma-1 sequence corresponds to
 CC the equivalent gamma-3 sequence (AAR49531) of a camel 2-chain Ig molecule
 CC (100 kDa) which lacks any light chains. The Ig has e.g. improved
 CC solubility and aggregate much less than heavy chains of 4-chain IgG. The
 CC IgG can be used normally for e.g. diagnosis, therapy, in vaccines, for
 CC isolation and purification of antigens and in the production of anti-
 CC idiotypic antibodies. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX SQ Sequence 18 AA;
 XX
 XX Query Match 100.0%; Score 23; DB 2; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 GQPR 4
 XX ||||
 XX 1 GQPR 4
 XX
 XX RESULT 36
 XX ABR57545
 XX ID ABR57545 standard; peptide; 22 AA.
 XX
 XX AC ABR57545;
 XX
 XX DT 04-AUG-2003 (first entry)
 XX
 XX DE Anti-angiogenic peptide RAND1.
 XX
 XX KW Cytostatic; Neupilin-1 receptor; NP-1 receptor; angiogenesis; cancer;
 XX Vascular Endothelial Growth Factor Receptor-2; VEGFR-2; PIGF; VEGF;
 XX Placental Growth Factor; Vascular Endothelial Growth Factor;
 XX anti-angiogenic.
 XX
 XX OS Unidentified.
 XX
 XX PN WO2003029275-A2.
 XX
 XX PD 10-APR-2003.
 XX
 XX PF 02-OCT-2002; 2002WO-US031386.
 XX
 XX PR 03-OCT-2001; 2001US-0326712P.
 XX
 XX PA (REGE-) REGENERON PHARM INC.
 XX (PROC) PROCTER & GAMBLE CO.
 XX
 XX PI Rosenbaum JS, Jones DR, Whitaker GB;
 XX WPI; 2003-371982/35.
 XX
 XX PT New anti-angiogenic peptides that are capable of binding to NP-1 or
 PT vascular endothelial growth factor receptor (VEGFR)-2/NP-1 complex,
 PT useful for treating diseases characterized by abnormal angiogenesis, such
 PT as cancer.
 XX
 XX PS Disclosure; Page 113; 115pp; English.
 XX
 XX CC The present invention relates to peptides that are capable of binding to
 CC Neupilin-1 (NP-1) receptor or the Vascular Endothelial Growth Factor
 CC Receptor (VEGFR)-2/NP-1 complex. The peptides are derived from a
 CC combination of peptides from Exon 6 of Placental Growth Factor (PIGF),
 CC coupled at the carboxyl terminus to either Exon 8 of Vascular Endothelial
 CC Growth Factor (VEGF) isoform 165 (VEGF165), also referred to as P6V8) or
 CC Exon 7 of PIGF (referred to as P6P7). The peptides and compositions are
 CC useful for treating diseases characterised by abnormal angiogenesis, such

CC as cancer. The present peptide is an anti-angiogenic peptide used to
 CC illustrate the invention
 XX
 SQ Sequence 22 AA;

Query Match 100.0%; Score 23; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 8 GQPR 11

RESULT 37
 AAP30407
 ID AAP30407 standard; peptide; 23 AA.

XX
 AC AAP30407;
 XX
 DT 25-MAR-2003 (revised)
 DT 16-AUG-2002 (revised)
 DT 04-APR-1992 (first entry)
 XX
 DE Sequence of residues 335-357 of immunoglobulin G (IgG).
 XX
 KW Cancer therapy; parasite infection; autoimmune disease; T-cell;
 natural killer cell.
 XX
 OS Synthetic.
 XX
 PN EP94233-A.
 XX
 PD 16-NOV-1983.
 XX
 PF 09-MAY-1983; 83EP-00302601.
 XX
 PR 11-MAY-1982; 82US-00377223.
 XX
 PA (SCRI) SCRIPPS CLINIC & RES FOUND.
 XX
 PI Weigle WO, Morgan EL;
 XX
 DR WPI; 1983-822296/47.
 XX
 PD 16-NOV-1983.
 XX
 PF 09-MAY-1983; 83EP-00302601.
 XX
 PR 11-MAY-1982; 82US-00377223.
 XX
 PA (SCRI) SCRIPPS CLINIC & RES FOUND.
 XX
 PI Weigle WO, Morgan EL;
 XX
 DR WPI; 1983-822296/47.
 XX
 PD Polypeptide(s) contg. sequence of IGG - useful for modulation of immune
 PT response in treating cancers, infections etc.
 XX
 PS Disclosure; Page 20; 54pp; English.

XX The inventors claim cpds. which include the 23 amino acid sequence
 CC represented by residues 335-357 of IGG to which is bonded, by amide
 CC formation, at the carboxyl terminal, homoserine or the lactone obtd. by
 CC dehydration of homoserine. The cpds. are useful for treating cancers,
 CC parasitic infections and many autoimmune diseases. Dose is 20 micrograms-
 CC 10 mg/kg daily parenterally or intraperitoneally. AAP30404-P30411 are
 CC illustrative of the cpds. of the invention. (Updated on 16-AUG-2002 to
 CC add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 23 AA;

Query Match 100.0%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 7 GQPR 10

RESULT 38
 AAP30405

ID AAP30405 standard; peptide; 23 AA.
 XX
 AC AAP30405;
 XX
 DT 25-MAR-2003 (revised)
 DT 16-AUG-2002 (revised)
 DT 04-APR-1992 (first entry)
 XX
 DE Sequence of residues 335-357 of immunoglobulin G (IgG).
 XX
 KW Cancer therapy; parasite infection; autoimmune disease; T-cell;
 natural killer cell.
 XX
 OS Synthetic.
 XX
 PN EP94233-A.
 XX
 PD 16-NOV-1983.
 XX
 PF 09-MAY-1983; 83EP-00302601.
 XX
 PR 11-MAY-1982; 82US-00377223.
 XX
 PA (SCRI) SCRIPPS CLINIC & RES FOUND.
 XX
 PI Weigle WO, Morgan EL;
 XX
 DR WPI; 1983-822296/47.
 XX
 PD Polypeptide(s) contg. sequence of IGG - useful for modulation of immune
 PT response in treating cancers, infections etc.
 XX
 PS Disclosure; Page 20; 54pp; English.

XX The inventors claim cpds. which include the 23 amino acid sequence
 CC represented by residues 335-357 of IGG to which is bonded, by amide
 CC formation, at the carboxyl terminal, homoserine or the lactone obtd. by
 CC dehydration of homoserine. The cpds. are useful for treating cancers,
 CC parasitic infections and many autoimmune diseases. Dose is 20 micrograms-
 CC 10 mg/kg daily parenterally or intraperitoneally. AAP30404-P30411 are
 CC illustrative of the cpds. of the invention. (Updated on 16-AUG-2002 to
 CC add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 23 AA;

Query Match 100.0%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 7 GQPR 10

RESULT 39
 AAP30404

ID AAP30404 standard; peptide; 23 AA.
 XX
 AC AAP30404;
 XX
 DT 25-MAR-2003 (revised)
 DT 16-AUG-2002 (revised)
 DT 04-APR-1992 (first entry)
 XX
 DE Sequence of residues 335-357 of immunoglobulin G (IgG).
 XX
 KW Cancer therapy; parasite infection; autoimmune disease; T-cell;
 natural killer cell.
 XX
 OS Synthetic.
 XX
 PN EP94233-A.

XX PD 16-NOV-1983.
 XX XX
 XX PF 09-MAY-1983; 83EP-00302601.
 XX XX
 XX PR 11-MAY-1982; 82US-00377223.
 XX XX
 XX PA (SCRI) SCRIPPS CLINIC & RES FOUND.
 XX XX
 XX PI Weigle WO, Morgan EL;
 XX XX
 XX DR WPI; 1983-822296/47.
 XX XX
 XX PT Polypeptide(s) contg. sequence of IGG - useful for modulation of immune
 XX response in treating cancers, infections etc.
 XX PS Disclosure; Page 20; 54pp; English.
 XX XX
 CC CC The inventors claim cpds. which include the 23 amino acid sequence
 CC represented by residues 335-357 of IGG to which is bonded, by amide
 CC formation, at the carboxyl terminal, homoserine or the lactone obtd. by
 CC dehydration of homoserine. The cpds. are useful for treating cancers,
 CC parasitic infections and many autoimmune diseases. Dose is 20 micrograms-
 CC 10 mg/kg daily parenterally or intraperitoneally. AAP30404-P30411 are
 CC illustrative of the cpds. of the invention. (Updated on 16-AUG-2002 to
 CC add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX XX
 XX SQ Sequence 23 AA;
 Query Match 100.0%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db ||||
 7 GQPR 10
 RESULT 41
 AAP30409
 ID AAP30409 standard; peptide; 23 AA.
 XX AC AAP30409;
 XX XX
 XX DT 25-MAR-2003 (revised)
 DT 16-AUG-2002 (revised)
 DT 04-APR-1992 (first entry)
 XX DE Sequence of residues 335-357 of immunoglobulin G (IGG).
 XX CC Cancer therapy; parasite infection; autoimmune disease; T-cell;
 KW natural killer cell.
 XX OS Synthetic.
 XX XX
 XX FN EP94233-A.
 XX PD 16-NOV-1983.
 XX XX
 XX PF 09-MAY-1983; 83EP-00302601.
 XX XX
 XX PR 11-MAY-1982; 82US-00377223.
 XX XX
 XX PA (SCRI) SCRIPPS CLINIC & RES FOUND.
 XX XX
 XX PI Weigle WO, Morgan EL;
 XX XX
 XX DR WPI; 1983-822296/47.
 XX XX
 XX PT Polypeptide(s) contg. sequence of IGG - useful for modulation of immune
 XX response in treating cancers, infections etc.
 XX PS Disclosure; Page 20; 54pp; English.
 XX XX
 CC CC The inventors claim cpds. which include the 23 amino acid sequence
 CC represented by residues 335-357 of IGG to which is bonded, by amide
 CC formation, at the carboxyl terminal, homoserine or the lactone obtd. by
 CC dehydration of homoserine. The cpds. are useful for treating cancers,
 CC parasitic infections and many autoimmune diseases. Dose is 20 micrograms-
 CC 10 mg/kg daily parenterally or intraperitoneally. AAP30404-P30411 are
 CC illustrative of the cpds. of the invention. (Updated on 16-AUG-2002 to
 CC add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX XX
 XX SQ Sequence 23 AA;
 Query Match 100.0%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db ||||
 7 GQPR 10
 RESULT 40
 AAP30406
 ID AAP30406 standard; peptide; 23 AA.
 XX AC AAP30406;
 XX XX
 XX DT 25-MAR-2003 (revised)
 DT 16-AUG-2002 (revised)
 DT 04-APR-1992 (first entry)
 XX DE Sequence of residues 335-357 of immunoglobulin G (IGG).
 XX CC Cancer therapy; parasite infection; autoimmune disease; T-cell;
 KW natural killer cell.
 XX OS Synthetic.
 XX XX
 XX FN EP94233-A.
 XX PD 16-NOV-1983.
 XX XX
 XX PF 09-MAY-1983; 83EP-00302601.
 XX XX
 XX PR 11-MAY-1982; 82US-00377223.
 XX XX
 XX PA (SCRI) SCRIPPS CLINIC & RES FOUND.
 XX XX
 XX PI Weigle WO, Morgan EL;
 XX XX
 XX DR WPI; 1983-822296/47.
 XX XX
 XX PT Polypeptide(s) contg. sequence of IGG - useful for modulation of immune
 XX response in treating cancers, infections etc.
 XX PS Disclosure; Page 20; 54pp; English.
 XX XX

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB ||||
 7 GQPR 10

RESULT 42
 ADH89371 ID ADH89371 standard; peptide; 23 AA.
 XX AC ADH89371;
 XX DT 15-APR-2004 (first entry)
 XX DE Human transferrin fusion protein-related peptide SeqID15.
 XX KW fusion protein; transferrin protein; glycosylation;
 KW antibody variable region; cytostatic; antibacterial; virucide;
 KW antiparasitic; immunosuppressive; antiarthritic; gene therapy;
 KW septic shock; endotoxin shock; cachexia syndrome; bacterial infection;
 KW viral infection; parasitic infection; neoplasm; autoimmune disease;
 KW arthritis; graft rejection; human.
 XX OS Homo sapiens.
 XX US2003226155-A1.
 XX PD 04-DEC-2003.
 XX PF 10-MAR-2003; 2003US-00384060.
 XX PR 30-AUG-2001; 2001US-0315745P.
 XX PR 30-NOV-2001; 2001US-0334059P.
 XX PR 30-AUG-2002; 2002US-0023149P.
 XX PR 30-AUG-2002; 2002US-0406977P.
 XX PA (BIOR-) BIOREXIS PHARM CORP.
 XX PI Sadeghi H, Prior CP, Turner A;
 XX WPI; 2004-022093/02.
 XX PT New fusion protein comprising a transferrin protein exhibiting reduced
 PT glycosylation fused to at least one antibody variable region, useful for
 PT preparing a composition for treating e.g., septic shock, neoplasm or
 PT autoimmune disease.
 XX PS Disclosure; SEQ ID NO 15; 82pp; English.
 XX CC This invention relates to a novel fusion protein which comprises a
 CC transferrin protein exhibiting reduced glycosylation fused to at least
 CC one antibody variable region. The invention may be useful for the
 CC development of compounds with cytostatic, antibacterial, virucide,
 CC antiparasitic, immunosuppressive or antiarthritic activity. In addition,
 CC the sequences disclosed may be useful for gene therapy. The fusion
 CC protein is useful for preparing a composition for treating a disease or
 CC disease symptom in a patient for example septic shock, endotoxin shock,
 CC cachexia syndromes associated with bacterial, viral or parasitic
 CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
 CC associated with treatment for preventing graft rejection. The present
 CC sequence is that of a peptide which is related to the invention.
 XX Sequence 23 AA;
 QY Query Match 100.0%; Score 23; DB 8; Length 23;
 DB Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 43
 ADS97551 ID ADS97551 standard; protein; 23 AA.
 XX AC ADS97551;
 XX DT 16-DEC-2004 (first entry)
 XX DE Dementia related secretogranin 1 peptide DRES-17.
 XX KW DRES-17; dementia related secretogranin 1; secretogranin 1;
 KW Alzheimer's disease; diagnosis; gene therapy; human; marker.
 XX OS Homo sapiens.
 XX WO2004082455-A2.
 XX PD 30-SEP-2004.
 XX PF 18-MAR-2004; 2004WO-BP002824.
 XX PR 18-MAR-2003; 2003EP-00005968.
 XX PR 07-JAN-2004; 2004EP-00000170.
 XX PA (BIOV-) BIOVISION AG.
 XX PI Lamping N, Zucht H, Selle H, Juergens M, Heine G, Hess R;
 PI Kellmann M, Lamerz J, Moehring T;
 XX WPI; 2004-718701/70.
 XX PT Detecting a neurological disease, particularly Alzheimer's disease,
 PT comprises determining at least one dementia related secretogranin 1
 PT (DRES) peptide, or at least one peptide corresponding to GeneBank
 PT Accession No NM001819.
 XX Claim 1; SEQ ID NO 17; 110pp; English.
 XX CC The present sequence is that of dementia related secretogranin 1 peptide
 CC DRES-17 (mass 2522.1 Da), corresponding to amino acids 253-275 of human
 CC secretogranin 1 ADS97579. The peptide can be used as a marker in claimed
 CC methods of the invention for detecting a neurological disease, preferably
 CC Alzheimer's disease (AD), or a predisposition to such a disease.
 CC Detection of AD is based on the finding that the concentration of certain
 CC peptides is changed in bodily fluid samples, especially in the
 CC cerebrospinal fluid, of AD patients relative to their concentration in
 CC control samples. A method for detecting a neurological disease, in
 CC particular a chronic dementia disease, especially AD or a predisposition
 CC to such a disease involves the detection of at least one DRES peptide
 CC ADS97535-ADS97578 and ADS97581-ADS97591 in a biological sample.
 CC Preferably, the peptide(s) is determined in combination with one or more
 CC peptides derived from chromogranin A ADS97606-ADS97619, secretogranin 2
 CC ADS97595-ADS97605 and/or secretogranin 5 ADS97592-ADS97594. The disease
 CC can be detected at an early stage e.g. in the diagnosis of mild cognitive
 CC impairment, or in neurological diseases other than AD, such as Lewy body
 CC dementia, vascular dementia or depression. Determination of the marker
 CC peptides is conducted by an activity, immunological, molecular
 CC biological, physical or chemical assay. Preferably the mass of the
 CC peptide is determined by mass spectrometry. Pharmaceutical products
 CC comprise the marker peptides, antibodies directed to the peptides,
 CC nucleic acids corresponding to the peptides, a ribozyme, antisense
 CC nucleic acid, triplex-forming nucleic acid or RNAi nucleic acid, peptide
 CC antagonists or peptide agonists for the therapy, diagnosis, prognosis or
 CC prophylaxis of neurological diseases, particularly AD. The marker
 CC peptides may be mutated at 1 or 2 amino acid positions corresponding to
 CC the non-mutated DRES sequence, or chemically or enzymatically modified,
 CC or post-translationally modified, preferably phosphorylated, sulfated,
 CC oxidised or C-terminally amidated, or have a pyroglutamate modification
 CC in an individual's biological sample.
 XX Sequence 23 AA;

Query Match 100.0%; Score 23; DB 8; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 3 GQPR 6

RESULT 44
 AAP30413
 ID AAP30413 standard; peptide; 24 AA.
 AC AAP30413;
 XX 25-MAR-2003 (revised)
 DT 16-AUG-2002 (revised)
 DT 04-APR-1992 (first entry)
 XX Sequence of residues 335-357 of immunoglobulin G (IgG) plus C-terminal homoserine.
 DE
 DE
 KW Cancer therapy; parasite infection; autoimmune disease; T-cell;
 KW natural killer cell.
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /label= H-Thr
 FT Misc-difference 24
 FT /label= homoserine
 FT /note= "optional"
 XX
 DN EP94233-A.
 XX
 PD 16-NOV-1983.
 XX
 PF 09-MAY-1983; 83EP-00302601.
 XX
 PR 11-MAY-1982; 82US-00377223.
 XX
 XX (SCRI) SCRIPPS CLINIC & RES FOUND.
 XX
 XX Weigle WO, Morgan EL;
 XX
 DR WPI; 1983-822296/47.
 XX
 XX Polypeptide(s) contg. sequence of IgG - useful for modulation of immune response in treating cancers, infections etc.
 PT
 PS Claim 9; Page 49; 54pp; English.
 XX
 CC The inventors claim cpds. which include the 23 amino acid sequence represented by residues 335-357 of IgG to which is bonded, by amide formation, at the carboxyl terminal, homoserine or the lactone obtd. by dehydration of homoserine. The cpds. are useful for treating cancers, parasitic infections and many autoimmune diseases. Dose is 20 micrograms-10 mg/kg daily parenterally or intraperitoneally. AAP30404-P30411 are illustrative of the cpds. of the invention. (Updated on 16-AUG-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX Sequence 24 AA;
 SQ

Query Match 100.0%; Score 23; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 7 GQPR 10

RESULT 45
 AAU89298
 ID AAU89298 standard; peptide; 25 AA.
 AC AAU89298;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Insulin/insulin-like growth factor receptor-binding peptide #1254.
 XX
 KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
 KW diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.
 XX
 OS Synthetic.
 XX
 PN WO200172771-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 29-MAR-2000; 2000WO-US008528.
 XX
 PR 29-MAR-2000; 2000WO-US008528.
 XX
 PA (DGIB-) DGI BIOTECHNOLOGIES LLC.
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
 PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
 PI Hansen PH, Ravera M, Hsiao K;
 XX
 DR WPI; 2002-025774/03.
 XX
 PT Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumors, comprises using peptides that bind to insulin or insulin-like growth factor receptors.
 PT
 PS Disclosure; Fig 2E; 390pp; English.
 XX
 CC The invention relates to a method of modulating insulin activity in mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are antagonists of the insulin-like growth factor-1 (IGF-1) receptor are useful for treating insulin-like growth factor (IGF)-sensitive tumours (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful in screening for compounds that bind to IR or IGF-1 receptor, potential therapeutics and research reagents. AAU88034-AAU90957 represent IR and/or IGF-1 receptor-binding peptides and related amino acid sequences of the invention
 CC
 XX Sequence 25 AA;
 SQ

Query Match 100.0%; Score 23; DB 5; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 12 GQPR 15

RESULT 46
 ABO23580
 ID ABO23580 standard; protein; 27 AA.
 XX
 AC ABO23580;
 XX

DT 04-SEP-2003 (first entry)
 XX Mycobacterium tuberculosis outlier protein #6.
 DE
 XX
 XX Candidate protein identification; pathogen; anti-infective;
 KW outlier protein; virulence protein; antigen; drug target protein;
 KW pathogenic organism; antimicrobial.
 XX
 XX Mycobacterium tuberculosis.
 OS
 XX US2003039963-A1.
 PN 27-FEB-2003.
 XX
 XX 30-MAR-2001; 2001US-00820843.
 PF 30-MAR-2001; 2001US-00820843.
 XX
 XX (BRAH/) BRAHMACHARI S K.
 PA (RAMA/) RAMACHANDRAN S.
 PA (NAND/) NANDI T.
 PA (BHIM/) BHIMARAO C.
 XX
 XX Brahmachari SK, Ramachandran S, Nandi T, Bhimmarao C;
 PI WPI; 2003-492159/46.
 DR
 XX
 XX Identifying candidate proteins useful as anti-infectives involves
 PT matching outlier protein sequences with protein sequences in databases.
 PT
 XX
 XX Example 7; Page 80; 117pp; English.
 PS
 XX The present invention relates to a method for identifying candidate
 CC proteins in pathogens useful as anti-infectives. The invention discloses
 CC a computational method which involves the calculation of several sequence
 CC attributes and their subsequent analysis results in the identification
 CC of outlier proteins in different pathogens. The method is useful for the
 CC identification of outlier proteins (e.g. virulence proteins, antigens or
 CC proteins used as drug targets) in pathogenic organisms. The method of the
 CC invention provides reproducible results as it does not depend on the
 CC variable biochemical characterisation of proteins. ABO23500-ABO23617
 CC represent outlier proteins identified from different pathogenic organisms
 XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 23; DB 7; Length 27;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db |||||
 2 GQPR 5
 RESULT 47
 AAW37936
 ID AAW37936 standard; peptide; 28 AA.
 AC
 XX
 XX 27-AUG-2003 (revised)
 DT 10-AUG-1998 (first entry)
 XX
 XX Herpes virus detection peptide.
 DE
 XX Herpes virus detection peptide; Kasopi's sarcoma-associated Herpes virus;
 KW vaccine; Herpes Simplex Virus I; Herpes Virus II; Human Cytomegalovirus;
 KW Varicella Zoster Virus; Marek's Disease Virus; Epstein Barr Virus;
 KW Herpes Virus IV.
 XX
 XX Synthetic.
 OS Human herpesvirus 8.
 OS
 XX

PN US5760175-A.
 XX
 PD 02-JUN-1998.
 XX
 PF 05-SEP-1996; 96US-00708893.
 XX
 PR 05-SEP-1996; 96US-00708893.
 XX
 PA (BIOV-) BIO-VIRUS RES INC.
 XX
 PI Golubev DB, Chaihorsky A;
 XX
 DR WPI; 1998-332242/29.
 XX
 PT New peptide homologous to Kasopi's Sarcoma-Associated Herpes Virus sub-
 PT units - is useful for the detection of, and vaccination against several
 PT herpes virus infections.
 XX
 PS Claim 1; Col 5-6; 4pp; English.
 XX
 CC This is the amino acid sequence of the novel Herpes virus detection
 CC peptide, which is homologous with the parts of the subunits of the
 CC Kasopi's sarcoma-associated Herpes virus. It is useful for use as a
 CC vaccine against pathogenic development of several herpes infections, e.g.
 CC Herpes Simplex Virus I and II, Human Cytomegalovirus, Varicella Zoster
 CC Virus, Marek's Disease Virus, Epstein Barr Virus and especially Kasopi's
 CC Sarcoma-Associated Herpes Virus. The peptide is also useful for the
 CC detection of herpes type-4 virus. (Updated on 27-AUG-2003 to correct OS
 CC field.)
 XX
 SQ Sequence 28 AA;
 Query Match 100.0%; Score 23; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db |||||
 24 GQPR 27
 RESULT 48
 AAY56879
 ID AAY56879 standard; peptide; 28 AA.
 AC
 XX
 XX AAY56879;
 DT 12-SEP-2003 (revised)
 DT 14-APR-2000 (first entry)
 XX
 XX Peptide in a vaccine against Kasopi's sarcoma-associated herpes virus.
 DE
 XX Immune response; herpes virus; vaccine.
 KW Human herpesvirus 8.
 XX
 OS Human herpesvirus 8.
 XX
 XX US6015566-A.
 PN
 XX
 PD 18-JAN-2000.
 XX
 XX 01-JUN-1998; 98US-00088154.
 PF
 XX
 PR 05-SEP-1996; 96US-00708893.
 XX
 XX (BIOV-) BIO-VIRUS RES INC.
 PA
 XX Golubev DB, Chaihorsky A;
 PI
 XX WPI; 2000-126310/11.
 DR
 XX Vaccine against herpes viruses, especially Kasopi's sarcoma-associated
 PT herpes virus, comprises specific peptide coupled to carrier protein.
 PT
 XX

PS Disclosure; Col 2; 5pp; English.

XX The invention provides a composition for generating an immune response to

CC a herpes virus. The composition comprises the present sequence conjugated

CC to a carrier is useful as a vaccine against various herpes viruses,

CC especially Kaposi's sarcoma-associated herpes virus. (Updated on 12-SEP-

CC 2003 to standardise OS field)

XX

SQ Sequence 28 AA;

Query Match 100.0%; Score 23; DB 3; Length 28;

Best Local Similarity 100.0%; Pred. No. 6.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GQPR 4

Db 24 GQPR 27

RESULT 49

ABO54482

ID ABO54482 standard; protein; 31 AA.

XX

AC ABO54482;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human genome derived single exon protein #716.

XX

KW Human; gene expression; single exon probe; microarray;

KW alternative splicing event; genomic alteration.

XX

OS Homo sapiens.

XX

PN US2003194704-A1.

XX

PD 16-OCT-2003.

XX

PF 03-APR-2002; 2002US-00029386.

XX

PR 03-APR-2002; 2002US-00029386.

XX

PA (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

XX

PI Penn SG, Rank DR, Hanzel DK;

XX

DR WPI; 2004-119264/12.

XX

PT New human genome-derived single exon nucleic acid probes useful for human

PT gene expression analysis, for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for

PT surveying tissues.

XX

PS Claim 45; SEQ ID NO 28116; 80pp; English.

XX

CC The invention relates to a nucleic acid probe for measuring human gene

CC expression, comprising any of the 27,400 fully defined nucleotide

CC sequences in the specification, or their complements or fragments, and

CC encoding at least 8 amino acids of any of the 6888 amino acid sequences

CC fully defined in the specification. The probe is a single exon probe that

CC hybridises under high stringency conditions to a nucleic acid molecule

CC expressed in human cells or tissues. Also included are a spatially-

CC addressable set of single exon nucleic acid probes for measuring human

CC gene expression (comprising a plurality of single exon nucleic acid

CC probes cited above, where each of the plurality of probes is separately

CC and addressably isolatable or amplifiable from the plurality), a single

CC exon microarray for measuring human gene expression, a method of

CC measuring human gene expression, a vector comprising the single exon

CC probe cited above, an ORF-encoded peptide comprising at least 8

CC contiguous amino acids of any of the above-mentioned amino acid

CC sequences (optionally with conservative amino acid substitutions), an

CC isolated antibody that binds specifically to a peptide cited above,

CC a method of selling and/or licensing single exon probes or microarrays to

CC a customer desiring to measure gene expression, a method of providing

CC human gene expression data by subscription, and a computer-readable

CC storage medium which contains a database having a plurality of records

CC (each record including data on the expression of a single exon probe

CC cited above. The probe, methods and apparatus are useful in gene

CC expression analysis. The probes may be used as tools for surveying

CC tissues to detect the presence of expressed messages that contain their

CC specific exon, or in constructing genome-derived single exon microarrays.

CC In addition, the probes are used in identifying and characterising

CC alternative splicing events, in detecting and characterising gross

CC alterations in the genomic locus that includes their exon, in assessing

CC smaller genomic alterations, in priming the synthesis of nucleic acids,

CC or in expressing the ORF-encoded peptide. The present sequence is a human

CC single exon probe protein of the invention. Note: The sequence data for

CC this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from USPTO at

CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 23; DB 8; Length 31;

Best Local Similarity 100.0%; Pred. No. 6.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GQPR 4

Db 28 GQPR 31

RESULT 50

AAB51356

ID AAB51356 standard; peptide; 33 AA.

XX

AC AAB51356;

XX

DT 09-APR-2001 (first entry)

XX

DE Mouse blood cell growth inhibiting factor related peptide SEQ ID NO:2.

XX

KW Mouse; blood cell growth inhibiting factor; BGIF; proliferation;

KW lymph-haematopoietic cell; lymph-haematopoietic system disease;

KW diagnosis.

XX

OS Mus musculus.

XX

PN JP2000300264-A.

XX

PD 31-OCT-2000.

XX

PF 14-APR-1999; 99JP-00107246.

XX

PR 14-APR-1999; 99JP-00107246.

XX

PS (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.

XX

DR WPI; 2001-141349/15.

XX

PT A protein with growth inhibiting activity to lymph-hematopoietic cells,

PT useful for the diagnosis and treatment of lymph-hematopoietic system

PT diseases.

XX

PS Example 2; Page 15; 21pp; Japanese.

XX

CC The present invention describes a mouse blood cell growth-inhibiting

CC factor (BGIF) protein derived from BMS (bone marrow stem cells) 2.4 cells

CC having inhibitory activity to the growth of lymph-haematopoietic cells.

CC The BGIF gene and protein are useful for the diagnosis and treatment of

CC lymph-haematopoietic system diseases. The present sequence represents an

CC amino acid sequence which is used in an example from the present

CC invention

SQ Sequence 33 AA;
 Query Match 100.0%; Score 23; DB 4; Length 33;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 13 GQPR 16
 RESULT 51
 AAY19644
 ID AAY19644 standard; protein; 35 AA.
 XX AC AAY19644;
 XX DT 14-JUL-1999 (first entry)
 XX DE SEQ ID NO 362 from WO9922243.
 XX KW Human secreted protein; cancer; tumour; neurodegenerative disorder;
 KW developmental abnormality; fetal deficiency; blood disorder; leukemia;
 KW immune system disease; autoimmune disease; hepatic disease;
 KW renal disease; lymphoma; inflammation; allergy; ischemic shock;
 KW Alzheimer's; cognitive disorder; schizophrenia; prostate disease;
 KW obesity; osteoclast; osteoporosis; arthritis; malignancy; testes disease;
 KW lung disease; thymus disease; digestive disorder; endocrine disorder;
 KW infection; AIDS.
 XX OS Homo sapiens.
 XX PN WO9922243-A1.
 XX PD 06-MAY-1999.
 XX XX 23-OCT-1998; 98WO-US022376.
 XX PR 24-OCT-1997; 97US-0062784P.
 XX PR 24-OCT-1997; 97US-0063088P.
 XX PR 24-OCT-1997; 97US-0063089P.
 XX PR 24-OCT-1997; 97US-0063090P.
 XX PR 24-OCT-1997; 97US-0063091P.
 XX PR 24-OCT-1997; 97US-0063092P.
 XX PR 24-OCT-1997; 97US-0063097P.
 XX PR 24-OCT-1997; 97US-0063098P.
 XX PR 24-OCT-1997; 97US-0063099P.
 XX PR 24-OCT-1997; 97US-0063100P.
 XX PR 24-OCT-1997; 97US-0063101P.
 XX PR 24-OCT-1997; 97US-0063109P.
 XX PR 24-OCT-1997; 97US-0063110P.
 XX PR 24-OCT-1997; 97US-0063111P.
 XX PR 24-OCT-1997; 97US-0063148P.
 XX PR 24-OCT-1997; 97US-0063386P.
 XX PR 24-OCT-1997; 97US-0063387P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX PI Feng P, Rosen CA, Ruben SM, Ni J, Wei Y, Soppet DR, Moore PA;
 PI Kayw H, Latleur DW, Olsen HS, Brewer LA, Shi Y, Ebner R, Young P;
 PI Greene JW, Florence KA, Florence C, Duan DR, Janat F, Endress GA;
 PI Carter KC;
 XX WPI; 1999-303069/25.
 XX PT New isolated human genes and the secreted polypeptides they encode.
 XX PS Disclosure; Page 482; 546pp; English.
 XX CC The specification describes human secreted proteins. The polynucleotides
 CC and their corresponding secreted polypeptides are useful for preventing,
 CC treating or ameliorating medical conditions, e.g. by protein or gene
 CC therapy. Pathological conditions can also be diagnosed by determining the

CC amount of the polypeptides in a sample or by determining the presence of
 CC mutations in the polynucleotides. Specific uses are described for each of
 CC the polynucleotides, based on which tissues they are most highly
 CC expressed in, and include developing products for the diagnosis or
 CC treatment of cancer, tumours, neurodegenerative disorders, developmental
 CC abnormalities and fetal deficiencies, blood disorders, leukemias,
 CC diseases of the immune system, autoimmune diseases, hepatic and renal
 CC disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's
 CC and cognitive disorders, schizophrenia, prostate diseases, obesity,
 CC disorders involving osteoclasts such as osteoporosis, arthritis or
 CC malignancies, diseases of testes, lung or thymus, digestive/endocrine
 CC disorders, infections and AIDS. The polypeptides are also useful for
 CC identifying their binding partners
 XX Sequence 35 AA;
 Query Match 100.0%; Score 23; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 3 GQPR 6
 RESULT 52
 AAY98355
 ID AAY98355 standard; peptide; 35 AA.
 XX AC AAY98355;
 XX DT 31-JUL-2000 (first entry)
 XX DE Alpha D peptide derived from TrkC SEQ ID NO:70.
 XX KW Alpha D peptide; Alpha D region; protein kinase; modulation; activity;
 KW cytostatic; anti-diabetic; anorectic; antiinflammatory; dermatological;
 KW immunosuppressive; immunomodulator; osteopathic; cardiant; vasotropic;
 KW antiarteriosclerotic; protein kinase modulator; cancer; proliferation;
 KW restenosis; atherosclerosis; skin disorder; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder; osteoporosis;
 KW autoimmune disease; immune disorder; cardiovascular disease.
 XX OS Homo sapiens.
 XX PN WO200018895-A1.
 XX PD 06-APR-2000.
 XX PR 24-SEP-1999; 99WO-US022106.
 XX PR 25-SEP-1998; 98US-00161094.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX PI Ben-Sasson SA;
 XX WPI; 2000-328722/28.
 XX PT Peptide derivatives of protein kinase alpha D regions which selectively
 PT modulate the activity of protein kinases.
 XX PS Claim 53; Fig 1; 148pp; English.
 XX CC The present invention describes a peptide derivative (A) of the protein
 CC kinase alpha D region comprising 5-30 amino acids, which modulates the
 CC activity of the protein kinase. AAY98286 to AAY98455 represent peptides
 CC derived from protein kinase alpha D regions, which are used in the
 CC exemplification of the present invention. The peptides have cytostatic,
 CC anti-diabetic, anorectic, antiinflammatory, dermatological, cardiant,
 CC immunosuppressive, immunomodulator, osteopathic, vasotropic and
 CC antiarteriosclerotic activities, and are protein kinase modulators. The

CC peptides can be used as test peptides to identify protein kinase
 CC modulators. They can also be used to modulate the activity of a protein
 CC kinase in a subject, and in a method of detecting a ligand that binds to
 CC the alpha D region of a protein kinase. They may be used to produce
 CC antibodies that bind to the alpha D region of a protein kinase. The
 CC peptides are useful in the treatment of diseases caused by over- or under
 CC -activity of a protein kinase, e.g. cancer, diseases caused by
 CC proliferation of smooth muscle (e.g. restenosis and atherosclerosis),
 CC skin disorders, diabetes, obesity, diseases of the central nervous
 CC system, inflammatory disorders, autoimmune diseases and other immune
 CC disorders, osteoporosis and cardiovascular diseases
 XX
 SQ Sequence 35 AA;

Query Match 100.0%; Score 23; DB 3; Length 35;

Best Local Similarity 100.0%; Pred. No. 7.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4

Db 26 GQPR 29

RESULT 53

AAW82815

ID AAW82815 standard; protein; 35 AA.

AC AAW82815;

XX

XX

DT 07-NOV-2001 (first entry)

XX

XX

DE Human immune/haematopoietic antigen SEQ ID NO:10408.

XX

XX

KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

KW Cytostatic; gene therapy; vaccine; metastasis.

XX

OS Homo sapiens.

XX

XX

PN WO200157182-A2.

XX

XX

PD 09-AUG-2001.

XX

XX

PF 17-JAN-2001; 2001WO-US001354.

XX

XX

PR 31-JAN-2000; 2000US-0179065P.

PR

PR 04-FEB-2000; 2000US-0180628P.

PR

PR 24-FEB-2000; 2000US-0184664P.

PR

PR 02-MAR-2000; 2000US-0186350P.

PR

PR 16-MAR-2000; 2000US-0189874P.

PR

PR 17-MAR-2000; 2000US-0190076P.

PR

PR 18-APR-2000; 2000US-0198123P.

PR

PR 19-MAY-2000; 2000US-0205515P.

PR

PR 07-JUN-2000; 2000US-0209467P.

PR

PR 28-JUN-2000; 2000US-0214886P.

PR

PR 30-JUN-2000; 2000US-0215135P.

PR

PR 07-JUL-2000; 2000US-0216647P.

PR

PR 07-JUL-2000; 2000US-0216880P.

PR

PR 11-JUL-2000; 2000US-0217487P.

PR

PR 11-JUL-2000; 2000US-0217496P.

PR

PR 14-JUL-2000; 2000US-0218290P.

PR

PR 26-JUL-2000; 2000US-0220963P.

PR

PR 26-JUL-2000; 2000US-0220964P.

PR

PR 14-AUG-2000; 2000US-0224518P.

PR

PR 14-AUG-2000; 2000US-0224519P.

PR

PR 14-AUG-2000; 2000US-0225213P.

PR

PR 14-AUG-2000; 2000US-0225214P.

PR

PR 14-AUG-2000; 2000US-0225266P.

PR

PR 14-AUG-2000; 2000US-0225267P.

PR

PR 14-AUG-2000; 2000US-0225268P.

PR

PR 14-AUG-2000; 2000US-0225270P.

PR

PR 14-AUG-2000; 2000US-0225447P.

PR

PR 14-AUG-2000; 2000US-0225757P.

PR

PR 14-AUG-2000; 2000US-0225758P.

PR

PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239355P.
 PR 13-OCT-2000; 2000US-023937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.

PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 11-DEC-2000; 2000US-0251990P.
 PR 05-JAN-2001; 2000US-0254097P.
 PR 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-483426/52.
 DR N-PSDB; AAK55596.
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.
 XX Claim 11; SEQ ID NO 10408; 3071pp + Sequence Listing; English.
 XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK34942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention
 XX Sequence 35 AA;
 XX Query Match 100.0%; Score 23; DB 4; Length 35;
 XX Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 GQPR 4
 XX |||||

Db 22 GQPR 25

RESULT 54
 AAU83474
 ID AAU83474 standard; peptide; 35 AA.
 XX AAU83474;
 AC AAU83474;
 XX 08-MAY-2002 (first entry)
 DT Human phospholipase A2 X peptide #1.
 DE XX
 DE XX
 DE XX
 KW Phospholipase A2; enzyme; PLA2; virucide; antirheumatic; antiarthritic;
 KW immunosuppressive; parvovirus; vlup; gene therapy;
 KW viral-associated disease; rheumatoid arthritis; systemic erythematosis;
 KW adult-onset Still's disease; polyarthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200200924-A2.
 XX
 XX 03-JAN-2002.
 XX
 XX 28-JUN-2001; 2001WO-CA000932.
 XX
 XX 28-JUN-2000; 2000CA-02310263.
 XX (NARE-) INST NAT RECH SCI.
 XX Tijssen P, Zadori Z;
 XX WPI; 2002-139932/18.
 XX
 PT New viral phospholipase A2 enzymes, useful in gene therapy for treating a
 PT subject viral-associated disease, e.g. rheumatoid arthritis, systemic
 PT erythematosis, adult-onset Still's disease or polyarthritis.
 XX
 XX Example 1; Fig 2; 107pp; English.
 XX
 CC The invention relates to an isolated viral polypeptide having
 CC phospholipase A2 (PLA2) activity (e.g. Vlp from parvoviruses) and the
 CC polynucleotides encoding them. Also included are a peptide that
 CC specifically binds a viral phospholipase A2 being (WY)-(CIVL)-G-x-(GP)-
 CC (GKNS)-x(8,14)-D-x(2)-(AC)-x(2)-x(2)-H-D-x(2)-Y. () = indicates the
 CC presence of one of the enclosed amino acids at this position; x = any
 CC amino acid; x(2) = a stretch of 2 amino acids; and x(8,14) = a stretch of
 CC 8-14 amino acids or Y-x-G-P-G-x(12)-D-x(2)-A-x(2)-H-D-x(2)-Y, a
 CC polypeptide that is an inactive variant of a viral polypeptide comprising
 CC an amino acid motif as detailed above, an antisense oligonucleotide
 CC complementary to the polynucleotide, a vector comprising the
 CC polynucleotide, a host cell comprising the vector, producing a
 CC recombinant virus comprising genetically engineered viral particles with
 CC the polynucleotide, fragment or vector, an antibody that bind to the
 CC protein, anti viral compounds which inhibit viral phospholipases. The
 CC polynucleotide is useful for gene therapy, and for improving a gene
 CC therapy vector. where the gene therapy vector is based on an adeno-
 CC associated virus. The antisense oligonucleotide is useful for inhibiting
 CC viral replication and/or infectivity in a subject, for manufacturing a
 CC medicament to treat the infectivity and/or replication of a virus in a
 CC subject or to treat viral-associated disease. The polypeptide is useful
 CC as an in vitro standard for measuring phospholipase A2 activity. The anti
 CC viral agent is used to decrease the infectivity and/or replication of a
 CC virus, e.g. parvovirus, in a subject. The anti-viral agent may also used
 CC to inhibit a viral phospholipase A2 in a subject in need of such therapy,
 CC where the subject has a viral-associated disease or disorder,
 CC particularly a disease associated with a parvovirus. The viral-associated
 CC disease includes rheumatoid arthritis, systemic erythematosis, adult-
 CC onset Still's disease or polyarthritis. The present sequence is a
 CC phospholipase peptide used to determine the motifs of the invention
 XX Sequence 35 AA;
 XX SQ

Query Match 100.0%; Score 23; DB 5; Length 35;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 15 GQPR 18

RESULT 55

ABW00600
 ID ABW00600 standard; peptide; 36 AA.

XX AC AEW00600;

XX DT 15-JAN-2004 (first entry)

XX DE BS136 epitope peptide #3.

XX KW Therapy; breast cancer; cytostatic; tumour; metastasis; BS136; EST;
 expressed sequence tag; epitope.

XX OS Unidentified.

XX PN US2003104364-A1.

XX PD 05-JUN-2003.

XX PF 25-JUN-1998; 98US-00104750.

XX PR 25-JUN-1997; 97US-00882369.

XX PA (BILL/) BILLINGEL P A.

XX PA (COHE/) COHEN M.

XX PA (COLP/) COLPITTS T L.

XX PA (FRIE/) FRIEDMAN P N.

XX PA (GRAN/) GRANADOS E N.

XX PA (KLAS/) KLAS M R.

XX PA (RUSS/) RUSSELL J C.

XX PA (STRO/) STROUPE S D.

XX PI Billengel PA, Cohen M, Colpitts TL, Friedman PN, Granados EN;
 Klass MR, Russell JC, Stroupe SD;

XX PI WPI; 2003-801225/75.

XX DR Novel BS136 polypeptide useful for detecting, diagnosing, staging,
 monitoring, prognosticating, preventing or treating breast diseases such
 as breast cancer.

XX PT Claim 7; Page 50; Opp; English.

XX PS The present invention relates to a novel BS136 polypeptide useful for
 detecting, diagnosing, preventing and treating breast diseases such as
 breast cancer. The invention is useful for preventing action of the
 tissue-specific BS136 polypeptide and for the therapeutic treatment of
 tumours and metastases. The present sequence is a BS136 epitope peptide

XX SQ Sequence 36 AA;

QY Query Match 100.0%; Score 23; DB 7; Length 36;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 GQPR 4
 19 GQPR 22

RESULT 56

AA86343
 ID AA86343 standard; peptide; 37 AA.

AC AA86343;

XX DT 19-APR-2000 (first entry)

XX DE Human gene 4-encoded protein fragment, SEQ ID NO:258.

XX DE Human; secreted protein; cancer; tumour; developmental abnormality;
 foetal deficiency; blood disorder; immune system disorder; inflammation;
 autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 therapy.

XX OS Homo sapiens.

XX PN WO966041-A1.

XX PD 23-DEC-1999.

XX PF 15-JUN-1999; 99WO-US013418.

XX PR 16-JUN-1998; 98US-0089507P.

XX PR 16-JUN-1998; 98US-0089508P.

XX PR 16-JUN-1998; 98US-0089509P.

XX PR 16-JUN-1998; 98US-0089510P.

XX PR 22-JUN-1998; 98US-0090112P.

XX PR 22-JUN-1998; 98US-0090113P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Ni J, Rosen CA, Wei Y, Young PE, Florence KA;
 Soppet DR, Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R;
 Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsoulis G;

XX PI WPI; 2000-106100/09.

XX PT New isolated human genes and the secreted polypeptides they encode,
 useful for diagnosis and treatment of e.g. cancers, neurological
 disorders, immune diseases, inflammation or blood disorders.

XX PT Disclosure; Page 12; 586pp; English.

XX CC AA297019 to AA297137 represent 94 isolated human secreted protein genes.
 AA86215 to AA86333 are the secreted proteins encoded by the 94 human
 genes. This sequence represents a fragment of one of the human secreted
 proteins. The genes and their corresponding secreted polypeptides are
 useful for preventing, treating or ameliorating medical conditions, e.g.,
 by protein or gene therapy. Also pathological conditions can be diagnosed
 by determining the amount of the new polypeptides in a sample or by
 determining the presence of mutations in the new genes. Specific uses are
 described for each of the 94 genes, based on which tissues they are most
 highly expressed in, and include developing products for the diagnosis or
 treatment of cancer, tumours, developmental abnormalities and foetal
 deficiencies, blood disorders, diseases of the immune system, autoimmune
 diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
 schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
 atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
 digestive/endocrine disorders, infections and AIDS. The polypeptides are
 also useful for identifying their binding partners. The sequences shown
 in AA86334 to AA86585 represent fragments of the secreted proteins

XX SQ Sequence 37 AA;

QY Query Match 100.0%; Score 23; DB 3; Length 37;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 GQPR 4
 16 GQPR 19

RESULT 57
 AB053488
 ID AB053488 standard; protein; 37 AA.
 XX
 AC AB053488;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Novel human secreted protein #4 fragment #3.
 XX
 KW Human; vaccine; immune system disorder; haematopoietic cell disorder;
 KW cancer; autoimmune disorder; rheumatoid arthritis; glomerulonephritis;
 KW HIV infection; anaemia; thrombocytopenia blood coagulation disorder;
 KW blood platelet disorder; wound; heart attack; myocardial infarction;
 KW stroke; scarring; asthma; graft-versus host rejection; inflammation;
 KW hyperproliferative disorder; lymphoproliferative disorder; arrhythmia;
 KW aberrant cellular division; cell proliferative disorder; angiogenesis;
 KW cardiovascular disorder; pulmonary heart disease; neovascularisation;
 KW hypertrophic scar; keloid; ocular disorder; diabetic retinopathy;
 KW uveitis; epithelial cell proliferation; neurological disease; apoptosis;
 KW Parkinson's disease; Alzheimer's disease; Huntington's chorea; ALS; AIDS;
 KW amyotrophic lateral sclerosis; toxin induced liver disease; septic shock;
 KW cachexia; anorexia; lung damage; infection.
 XX
 OS Homo sapiens.
 XX
 PN US2003065151-A1.
 XX
 PD 03-APR-2003.
 XX
 PF 04-APR-2002; 2002US-00115123.
 XX
 PR 16-JUN-1998; 98US-0089507P.
 PR 16-JUN-1998; 98US-0089508P.
 PR 16-JUN-1998; 98US-0089509P.
 PR 16-JUN-1998; 98US-0089510P.
 PR 22-JUN-1998; 98US-0090112P.
 PR 22-JUN-1998; 98US-0090113P.
 PR 15-JUN-1999; 99WO-US013418.
 PR 14-DEC-1999; 99US-00461325.
 XX
 (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Ni J, Rosen CA, Wei Y, Young P, Florence K, Soppet DR;
 PI Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R, Lafleur DW;
 PI Olsen H, Shi Y, Moore PA, Komatsoulis G;
 XX
 DR WPI; 2003-531736/50.
 XX
 PT Novel antibody that binds specifically to a HCEJQ69 protein, useful for
 PT detecting the presence of a protein in a biological sample, and for
 PT treating cancers, autoimmune disorders and HIV infection.
 XX
 PS Disclosure; Page 5; 176pp; English.
 XX
 CC The invention relates to an isolated antibody or its fragment that
 CC specifically binds to a protein. The antibody is useful for detecting a
 CC protein in a biological sample, by contacting the biological sample with
 CC the antibody or its fragment and detecting the protein in the biological
 CC sample. The antibody is useful for purifying, detecting and targeting the
 CC human secreted proteins, including both in vitro and in vivo diagnostic
 CC and therapeutic methods. The antibody is useful for immunophenotyping of
 CC cell lines in biological samples and in antibody-based therapies for
 CC treating, inhibiting and preventing diseases, disorders or conditions
 CC associated with aberrant expression and/or activity of the above
 CC proteins. The antibody is useful for treating deficiencies or disorders
 CC of immune system and haematopoietic cells, for increasing differentiation
 CC and proliferation of haematopoietic cells, for treating immune
 CC deficiencies or disorders e.g. cancers, autoimmune disorders (such as
 CC rheumatoid arthritis and glomerulonephritis), HIV infection, anaemia and
 CC thrombocytopenia and as a marker for a particular immune system disease
 CC or disorder. The antibody is also useful for treating blood coagulation
 CC disorders, blood platelet disorders, wounds, heart attacks (infarction),

CC strokes, scarring and asthma. The antibody is also useful for treating or
 CC preventing graft-versus host rejection, for modulating inflammation, for
 CC treating hyperproliferative disorders e.g. lymphoproliferative disorders
 CC and cancers, for inhibiting aberrant cellular division and for treating
 CC cell proliferative disorders. The antibody is also useful for treating
 CC cardiovascular disorders e.g. pulmonary heart disease and arrhythmia,
 CC disorders associated with neovascularisation and angiogenesis, for
 CC treating hypertrophic scars and keloids, ocular disorders e.g. diabetic
 CC retinopathy and uveitis, for wound healing and disorders of epithelial
 CC cell proliferation. The antibody is also useful for treating neurological
 CC diseases e.g. Parkinson's disease, Alzheimer's disease, Huntington's
 CC chorea and amyotrophic lateral sclerosis (ALS), diseases associated with
 CC increased apoptosis e.g. AIDS, toxin induced liver disease, septic shock,
 CC cachexia and anorexia, for preventing and healing damage to lungs and for
 CC treating infectious diseases. The present sequence represents the amino
 CC acid sequence of a novel human secreted protein fragment. Note: the
 CC specification data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?DocID=20030065151
 XX
 SQ Sequence 37 AA;
 Query Match 100.0%; Score 23; DB 6; Length 37;
 Best Local Similarity 100.0%; Pred. No. 7.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 16 GQPR 19
 RESULT 58
 AB023432
 ID AB023432 standard; peptide; 38 AA.
 XX
 AC AB023432;
 XX
 DT 04-SEP-2003 (first entry)
 XX
 DE Amino acid sequence #72 associated with human secreted proteins.
 XX
 KW Human; secreted protein; cancer; liver disorder; hepatitis;
 KW neural disorder; Alzheimer's disease; cytostatic; neuroprotective;
 KW hepatotropic; nootropic.
 XX
 OS Homo sapiens.
 XX
 PN US2003050455-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 06-FEB-2001; 2001US-00776724.
 XX
 PR 16-JUL-1997; 97US-0052661P.
 PR 16-JUL-1997; 97US-0052870P.
 PR 16-JUL-1997; 97US-0052871P.
 PR 16-JUL-1997; 97US-0052872P.
 PR 16-JUL-1997; 97US-0052873P.
 PR 16-JUL-1997; 97US-0052874P.
 PR 16-JUL-1997; 97US-0052875P.
 PR 22-JUL-1997; 97US-0053440P.
 PR 22-JUL-1997; 97US-0053441P.
 PR 22-JUL-1997; 97US-0053442P.
 PR 18-AUG-1997; 97US-0056359P.
 PR 15-JUL-1998; 98WO-US014613.
 PR 14-JAN-1999; 99US-00229982.
 PR 08-FEB-2000; 2000US-0180909P.
 PR 26-SEP-2000; 2000US-0069688.
 XX
 (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.

PA	(NIJ/) NI J.	18-AUG-1997;	97US-0055724P.
PA	(FENG/) FENG P.	18-AUG-1997;	97US-0055725P.
PA	(FLO/) FLORENCE K A.	18-AUG-1997;	97US-0055726P.
PA	(HUJ/) HU J.	18-AUG-1997;	97US-0055946P.
PA	(FERR/) FERRIE A M.	18-AUG-1997;	97US-0055952P.
PA	(YUGG/) YU G. G.	18-AUG-1997;	97US-0055983P.
PA	(DUAN/) DUAN R. D.	18-AUG-1997;	97US-0055989P.
PA	(JANA/) JANAT F.	18-AUG-1997;	97US-0056359P.
XX		15-JUL-1998;	98MO-US014613.
PI	Ruben SM, Rosen CA, Young PE, Greene JM, Ni J, Feng P;	14-JAN-1999;	99US-00229982.
PI	Florence KA, Hu J, Ferrie AM, Yu G, Duan RD, Janat F;	08-FEB-2000;	2000US-0180909P.
XX		26-SEP-2000;	2000US-00669688.
DR	WPI; 2003-492322/46.	06-FEB-2001;	2001US-00776724.
XX			
PT	New nucleic acid molecule, useful for preparing a medicament for		
PT	preventing, treating or ameliorating a medical condition e.g., cancer,		
PT	liver disorders such as hepatitis or neural disorders.		
XX			
PS	Disclosure; Page 29; 275pp; English.		
XX			
CC	The present invention relates to the isolation of novel human secreted		
CC	proteins and the polynucleotide sequences encoding them. The invention		
CC	also discloses vectors, host cells, antibodies, and recombinant methods		
CC	for producing human secreted proteins. The polypeptide and polynucleotide		
CC	sequences for the secreted proteins are useful for preparing a medicament		
CC	for preventing, treating or ameliorating medical conditions such as		
CC	cancer, liver disorders (e.g. hepatitis), and neural disorders (e.g.		
CC	Alzheimer's disease). ABO23361-ABO23499 represent amino acid sequences		
CC	associated with the human secreted proteins of the invention		
XX			
SQ	Sequence 38 AA;		
	Query Match	100.0%;	Score 23; DB 7; Length 38;
	Best Local Similarity	100.0%;	Pred. No. 8.1e+02;
	Matches	4; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GQPR 4		
DB	35 GQPR 38		
RESULT 59			
ID	ADR20820		
XX	ADR20820 standard; peptide; 38 AA.		
XX			
AC	ADR20820;		
XX			
DT	21-OCT-2004 (first entry)		
XX			
DE	Human secreted protein fragment from clone HMADU73 #1.		
XX			
XX	secreted protein; cancer; neurodegenerative disorder; cytostatic;		
KW	neuroprotective; gene therapy; IGF Fc region; fusion protein; human.		
XX			
OS	Homo sapiens.		
XX			
PN	US2004146893-A1.		
XX			
PD	29-JUL-2004.		
XX			
XX			
PF	15-OCT-2003; 2003US-00684496.		
XX			
XX	16-JUL-1997; 97US-0052661P.		
PR	16-JUL-1997; 97US-0052870P.		
PR	16-JUL-1997; 97US-0052871P.		
PR	16-JUL-1997; 97US-0052872P.		
PR	16-JUL-1997; 97US-0052873P.		
PR	16-JUL-1997; 97US-0052874P.		
PR	16-JUL-1997; 97US-0052875P.		
PR	22-JUL-1997; 97US-0053440P.		
PR	22-JUL-1997; 97US-0053441P.		
PR	22-JUL-1997; 97US-0053442P.		
PR	18-AUG-1997; 97US-0055683P.		
PR			
PA	(TOYM) TOYOBO KK.		
PA	(NAKA/) NAKAMURA T.		

PA	(NIJ/) NI J.	18-AUG-1997;	97US-0055724P.
PA	(FENG/) FENG P.	18-AUG-1997;	97US-0055725P.
PA	(FLO/) FLORENCE K A.	18-AUG-1997;	97US-0055726P.
PA	(HUJ/) HU J.	18-AUG-1997;	97US-0055946P.
PA	(FERR/) FERRIE A M.	18-AUG-1997;	97US-0055952P.
PA	(YUGG/) YU G. G.	18-AUG-1997;	97US-0055988P.
PA	(DUAN/) DUAN R. D.	18-AUG-1997;	97US-0056359P.
PA	(JANA/) JANAT F.	18-AUG-1997;	97US-0056361P.
XX		15-JUL-1998;	98MO-US014613.
PI	Ruben SM, Rosen CA, Young PE, Greene JM, Ni J, Feng P;	14-JAN-1999;	99US-00229982.
PI	Florence KA, Hu J, Ferrie AM, Yu G, Duan RD, Janat F;	08-FEB-2000;	2000US-0180909P.
XX		26-SEP-2000;	2000US-00669688.
DR	WPI; 2003-492322/46.	06-FEB-2001;	2001US-00776724.
XX			
PT	New nucleic acid molecule, useful for preparing a medicament for		
PT	preventing, treating or ameliorating a medical condition e.g., cancer,		
PT	liver disorders such as hepatitis or neural disorders.		
XX			
PS	Disclosure; Page 29; 275pp; English.		
XX			
CC	The present invention relates to the isolation of novel human secreted		
CC	proteins and the polynucleotide sequences encoding them. The invention		
CC	also discloses vectors, host cells, antibodies, and recombinant methods		
CC	for producing human secreted proteins. The polypeptide and polynucleotide		
CC	sequences for the secreted proteins are useful for preparing a medicament		
CC	for preventing, treating or ameliorating medical conditions such as		
CC	cancer, liver disorders (e.g. hepatitis), and neural disorders (e.g.		
CC	Alzheimer's disease). ABO23361-ABO23499 represent amino acid sequences		
CC	associated with the human secreted proteins of the invention		
XX			
SQ	Sequence 38 AA;		
	Query Match	100.0%;	Score 23; DB 7; Length 38;
	Best Local Similarity	100.0%;	Pred. No. 8.1e+02;
	Matches	4; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GQPR 4		
DB	35 GQPR 38		
RESULT 59			
ID	ADR20820		
XX	ADR20820 standard; peptide; 38 AA.		
XX			
AC	ADR20820;		
XX			
DT	21-OCT-2004 (first entry)		
XX			
DE	Human secreted protein fragment from clone HMADU73 #1.		
XX			
XX	secreted protein; cancer; neurodegenerative disorder; cytostatic;		
KW	neuroprotective; gene therapy; IGF Fc region; fusion protein; human.		
XX			
OS	Homo sapiens.		
XX			
PN	US2004146893-A1.		
XX			
PD	29-JUL-2004.		
XX			
XX			
PF	15-OCT-2003; 2003US-00684496.		
XX			
XX	16-JUL-1997; 97US-0052661P.		
PR	16-JUL-1997; 97US-0052870P.		
PR	16-JUL-1997; 97US-0052871P.		
PR	16-JUL-1997; 97US-0052872P.		
PR	16-JUL-1997; 97US-0052873P.		
PR	16-JUL-1997; 97US-0052874P.		
PR	16-JUL-1997; 97US-0052875P.		
PR	22-JUL-1997; 97US-0053440P.		
PR	22-JUL-1997; 97US-0053441P.		
PR	22-JUL-1997; 97US-0053442P.		
PR	18-AUG-1997; 97US-0055683P.		
PR			
PA	(TOYM) TOYOBO KK.		
PA	(NAKA/) NAKAMURA T.		

CC suppressing and activin or inhibin related activities. The proteins (and
 CC antibodies raised against them) and nucleic acids are therefore useful in
 CC the diagnosis and treatment of diseases and disorders such as cancer,
 CC central and peripheral nervous system diseases and neuropathies,
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular
 CC diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders,
 CC thrombocytopaenia, stem cell disorders, aplastic anaemia, for
 CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
 CC growth, and in tissue repair, healing of burns, incisions, ulcers, for
 CC treating osteoporosis, osteoarthritis, bone degenerative disorders, or
 CC periodontal disease, lung or liver fibrosis, reperfusion injury in
 CC various tissues, various immune deficiencies and disorders including
 CC severe combined immunodeficiency (SCID), bacterial or fungal infections,
 CC autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis,
 CC diabetes mellitus, myasthenia gravis), allergic reactions and conditions,
 CC such as asthma or other respiratory problems, coagulation disorders,
 CC haemophilia, septic shock, sepsis, arthritis, nephritis and inflammatory
 CC bowel disease, viral infection and are useful in altering bodily
 CC characteristics. The present sequence represents a novel protein of the
 CC invention
 XX
 SQ Sequence 41 AA;

Query Match 100.0%; Score 23; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 29 GQPR 32

RESULT 63
 AMM37357
 ID AAM37357 standard; protein; 41 AA.
 XX
 AC AAM37357;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Peptide #11394 encoded by probe for measuring placental gene expression.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200157272-A2.
 XX
 PD 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.
 XX
 XX 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 XX WPI; 2001-488897/53.
 DR
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 PT
 XX Claim 27; SEQ ID NO 37626; 654bp; English.
 PS
 XX

CC The present invention relates to single exon nucleic acid probes (SENP:
 CC see AA131315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders
 XX
 SQ Sequence 41 AA;

Query Match 100.0%; Score 23; DB 4; Length 41;
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 DB 12 GQPR 15

RESULT 64
 AAM91448
 ID AAM91448 standard; protein; 41 AA.

XX
 AC AAM91448;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen SEQ ID NO:19041.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis.
 XX
 OS Homo sapiens.
 XX
 PN WO200157182-A2.

XX 09-AUG-2001.
 XX 17-JAN-2001; 2001WO-US001354.
 XX
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 22-AUG-2000; 2000US-0227182P.


```

ID  AA064399 standard; protein; 41 AA.
XX  AC
XX  AA064399;
XX  DT
XX  05-NOV-2001 (first entry)
XX  DE Human brain expressed single exon probe encoded protein SEQ ID NO: 36504.
XX  DE Human; brain expressed exon; gene expression analysis; probe; microarray;
XX  KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX  KW Homo sapiens.
XX  OS
XX  WO200157275-A2.
XX  PN
XX  09-AUG-2001.
XX  PD
XX  30-JAN-2001; 2001WO-US000667.
XX  PF
XX  04-FEB-2000; 2000US-0180312P.
XX  PR 26-MAY-2000; 2000US-0207456P.
XX  PR 30-JUN-2000; 2000US-00608408.
XX  PR 03-AUG-2000; 2000US-00632366.
XX  PR 21-SEP-2000; 2000US-0234687P.
XX  PR 27-SEP-2000; 2000US-0236359P.
XX  PR 04-OCT-2000; 2000GB-00024263.
XX  PA (MOLE-) MOLECULAR DYNAMICS INC.
XX  PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX  WPI; 2001-483446/52.
XX  DR
XX  Single exon nucleic acid probes for analyzing gene expression in human
XX  PT brains.
XX  PT
XX  Example 4; SEQ ID NO 36504; 650pp + Sequence Listing; English.
XX  PS
XX  The present invention provides a number of single exon nucleic acid
XX  CC probes which are derived from genomic sequences expressed in the human
XX  CC brain. They can be used to measure gene expression in brain cell samples,
XX  CC which may enable the diagnosis and improved treatment of nervous system
XX  CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX  CC epilepsy and cancers. The present sequence is a protein encoded by one of
XX  CC the probes of the invention
XX  CC
XX  Sequence 41 AA;
XX  Query Match 100.0%; Score 23; DB 4; Length 41;
XX  Best Local Similarity 100.0%; Pred. No. 8.7e+02;
XX  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  QY 1 GQPR 4
XX  DB 12 GQPR 15
XX  RESULT 66
XX  ABG58845
XX  ID ABG58845 standard; peptide; 41 AA.
XX  AC
XX  ABG58845;
XX  DT 25-FEB-2003 (first entry)
XX  DE Human liver peptide, SEQ ID No 37493.
XX  DE
XX  KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX  KW hypercholesterolaemia; coronary heart disease.
XX  OS Homo sapiens.
XX  OS
XX  WO200157273-A2.
XX  PN

XX  AA064399 standard; protein; 41 AA.
XX  AC
XX  AA064399;
XX  DT
XX  05-NOV-2001 (first entry)
XX  DE Human brain expressed single exon probe encoded protein SEQ ID NO: 36504.
XX  DE Human; brain expressed exon; gene expression analysis; probe; microarray;
XX  KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX  KW Homo sapiens.
XX  OS
XX  WO200157275-A2.
XX  PN
XX  09-AUG-2001.
XX  PD
XX  30-JAN-2001; 2001WO-US000667.
XX  PF
XX  04-FEB-2000; 2000US-0180312P.
XX  PR 26-MAY-2000; 2000US-0207456P.
XX  PR 30-JUN-2000; 2000US-00608408.
XX  PR 03-AUG-2000; 2000US-00632366.
XX  PR 21-SEP-2000; 2000US-0234687P.
XX  PR 27-SEP-2000; 2000US-0236359P.
XX  PR 04-OCT-2000; 2000GB-00024263.
XX  PA (MOLE-) MOLECULAR DYNAMICS INC.
XX  PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX  WPI; 2001-488998/53.
XX  DR
XX  Human genome-derived single exon nucleic acid probes useful for analyzing
XX  PT gene expression in human adult liver.
XX  PT
XX  Claim 27; SEQ ID NO 37493; 658pp; English.
XX  PS
XX  The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX  CC measuring human gene expression in a sample derived from human adult
XX  CC liver, comprising one of 13109 defined nucleotide sequences given in the
XX  CC specification (or complements/ fragments). The probe hybridises at high
XX  CC stringency to a nucleic acid molecule expressed in the human adult liver.
XX  CC (I) may be used for predicting, measuring and displaying gene expression
XX  CC in samples derived from human adult liver. The genes identified may be
XX  CC involved in genetic liver diseases such as cirrhosis,
XX  CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX  CC associated with coronary heart disease. ABG47348-ABG5930 represent human
XX  CC liver single exon encoded peptides of the invention. Note: The sequence
XX  CC information for this patent does not appear in the printed specification
XX  CC but was obtained in electronic format directly from WIPO at
XX  CC ftp.wipo.int/pub/published_pct_sequences
XX  CC
XX  Sequence 41 AA;
XX  Query Match 100.0%; Score 23; DB 4; Length 41;
XX  Best Local Similarity 100.0%; Pred. No. 8.7e+02;
XX  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  QY 1 GQPR 4
XX  DB 12 GQPR 15
XX  RESULT 67
XX  ABG80821
XX  ID ABG80821 standard; protein; 42 AA.
XX  AC
XX  ABG80821;
XX  DT 29-NOV-2002 (first entry)
XX  DE
XX  DE Rat SP-A mutant protein E195Q.
XX  KW
XX  KW Scaffold protein; C-type lectin-like domain; CTLD; alpha-helix;
XX  KW beta-strand; connecting segment; 14loop region; tetranectin;
XX  KW ligand-binding specificity; human; mouse; rat; chicken; mutant; mutein.
XX  OS
XX  OS Rattus rattus.
XX  OS Synthetic.
XX  PN
XX  WO200248189-A2.
XX  XX
XX  20-JUN-2002.
XX  PF
XX  13-DEC-2001; 2001WO-DK000825.
XX  XX

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PR 13-DEC-2000; 2000DK-00001872.
 PR 28-FEB-2001; 2001US-0272098P.
 XX (BORE-) BOREAN PHARMA AS.
 PA Etzerodt M, Holtet TL, Gravarsen NJH, Thogersen HC;
 PI WPI; 2002-6432278/69.
 XX
 XX Protein comprising a variant of model C-type lectin-like domains (CTLDB),
 PT in which alpha helices, beta-strands, connecting segments are conserved
 PT to maintain CTLDB scaffold structure, while the loop region is altered.
 XX
 XX Claim 1; Page 17; 168pp; English.
 PS
 CC The present invention relates to a new protein with scaffold structure of
 CC C-type lectin-like domains (CTLDB). The invention comprises a variant of a
 CC model CTLDB where alpha-helices and beta-strands and connecting segments
 CC are conserved such that scaffold structure of C-type lectin-like domains
 CC (CTLDB) is substantially maintained, while the 14loop region is altered by
 CC amino acid substitution, deletion, insertion or their combination. The
 CC invention is useful for preparing a library of nucleotide sequences
 CC encoding related proteins by randomising part or all of the nucleic acid
 CC sequence encoding the loop region of its CTLDB. The artificial CTLDB
 CC protein products are preferable to antibody derivatives as each binding
 CC site is a single structurally autonomous protein domain. When used as
 CC components of compositions to be used for in vivo diagnostic or
 CC therapeutic purposes, artificial CTLDB protein products constructed on the
 CC basis of human CTLDBs are virtually identical to the corresponding natural
 CC CTLDB protein already present in the body and are therefore less
 CC immunogenic to the patient. They also have a smaller size, and thus
 CC provide tissue penetration and distribution, as well as shorter half life
 CC in circulation. Since murine and human tetranectin are identical in
 CC structure, straightforward swapping of polypeptide segments defining
 CC ligand-binding specificity between murine and human tetranectin
 CC derivatives may be achieved. The present amino acid sequence represents a
 CC mutant protein of the invention
 XX
 SQ Sequence 42 AA;
 Query Match 100.0%; Score 23; DB 5; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 29 GQPR 32
 XX
 RESULT 68
 ADS97549
 ID ADS97549 standard; protein; 42 AA.
 XX
 AC ADS97549;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Dementia related secretogranin 1 peptide DRES-15.
 XX
 KW DRES-15; dementia related secretogranin 1; secretogranin 1;
 KW Alzheimer's disease; diagnosis; gene therapy; human; marker.
 XX
 OS Homo sapiens.
 XX
 PN WO2004082455-A2.
 XX
 PD 30-SEP-2004.
 XX
 PF 18-MAR-2004; 2004WO-EP002824.
 XX
 PF 18-MAR-2003; 2003EP-00005968.
 PR 07-JAN-2004; 2004EP-00000170.
 XX
 XX

PA (BIOV-) BIOVISION AG.
 XX Lampung N, Zucht H, Selle H, Juergens M, Heine G, Hess R;
 PI Kellmann M, Lamerz J, Moehring T;
 XX WPI; 2004-718701/70.
 XX
 XX Detecting a neurological disease, particularly Alzheimer's disease,
 PT comprises determining at least one dementia related secretogranin 1
 PT (DRES) peptide, or at least one peptide corresponding to Genbank
 PT Accession No NM001819.
 XX
 PS Claim 1; SEQ ID NO 15; 110pp; English.
 XX
 CC The present sequence is that of dementia related secretogranin 1 peptide
 CC DRES-15 (mass 4583.1 Da), corresponding to amino acids 217-258 of human
 CC secretogranin 1 ADS97579 and optionally including a phosphorylated or
 CC sulfated residue. The peptide can be used as a marker in claimed methods
 CC of the invention for detecting a neurological disease, preferably
 CC Alzheimer's disease (AD), or a predisposition to such a disease.
 CC Detection of AD is based on the finding that the concentration of certain
 CC peptides is changed in bodily fluid samples, especially in the
 CC cerebrospinal fluid, of AD patients relative to their concentration in
 CC control samples. A method for detecting a neurological disease, in
 CC particular a chronic dementia disease, especially AD or a predisposition
 CC to such a disease involves the detection of at least one DRES peptide
 CC ADS97535-ADS97578 and ADS97581-ADS97591 in a biological sample.
 CC Preferably, the peptide(s) is determined in combination with one or more
 CC peptides derived from chromogranin A ADS97606-ADS97619, secretogranin 2
 CC ADS97595-ADS97605 and/or secretogranin 5 ADS97592-ADS97594. The disease
 CC can be detected at an early stage e.g. in the diagnosis of mild cognitive
 CC impairment, or in neurological diseases other than AD, such as Lewy body
 CC dementia, vascular dementia or depression. Determination of the marker
 CC peptides is conducted by an activity, immunological, molecular
 CC biological, physical or chemical assay. Preferably the mass of the
 CC peptide is determined by mass spectrometry. Pharmaceutical products
 CC comprise the marker peptides, antibodies directed to the peptides,
 CC nucleic acids corresponding to the peptides, a ribozyme, antisense
 CC nucleic acid, triplex-forming nucleic acid or RNAi nucleic acid, peptide
 CC antagonists or peptide agonists for the therapy, diagnosis, prognosis or
 CC prophylaxis of neurological diseases, particularly AD. The marker
 CC peptides may be mutated at 1 or 2 amino acid positions corresponding to
 CC the non-mutated DRES sequence, or chemically or enzymatically modified,
 CC or post-translationally modified, preferably phosphorylated, sulfated,
 CC oxidised or C-terminally amidated, or have a pyroglutamate modification
 CC in an individual's biological sample.
 XX
 SQ Sequence 42 AA;
 Query Match 100.0%; Score 23; DB 8; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 39 GQPR 42
 XX
 RESULT 69
 AAR95499
 ID AAR95499 standard; peptide; 43 AA.
 XX
 AC AAR95499;
 XX
 DT 06-NOV-1996 (first entry)
 XX
 DE E85, monoclonal antibody SM-3 derived antigen binding peptide.
 XX
 KW Abtide; prostate specific mucin antigen; human prostate cancer; LNCap;
 KW diagnostic; detection; imaging; tumour; phage; peptide library; breast;
 KW polymorphic; epithelial.
 XX
 OS Synthetic.

XX PN W09609411-A1.
 XX PD 28-MAR-1996.
 XX PF 20-SEP-1995; 95WO-US011934.
 XX PR 21-SEP-1994; 94US-00310192.
 XX PR 07-JUN-1995; 95US-00488161.
 XX PA (CYTO-) CYTOGEN CORP.
 XX PI Alvarez VL;
 XX PS WPI; 1996-188471/19.
 XX PT New isolated peptide(s) with specific binding activities - obtd. by
 PT screening random peptide libraries, for use in diagnostic and therapeutic
 PT compens.
 XX PS Claim 39; Page 78; 106pp; English.
 XX CC AAR95459-R95509 are antigen binding peptides ("abtides") derived from the
 CC monoclonal antibody SM-3 which recognises a specific polymorphic
 CC epithelial mucin tumour antigen found on human breast cancer cells. The
 CC abtides are identified from random peptide libraries using specific
 CC ligand binding. Abtides mimic the binding specificity of large molecules
 CC such as antibodies and receptors but have a much smaller size allowing
 CC their production at a lower cost and reducing the extent of their
 CC immunogenicity aiding in vivo delivery. The abtides are useful for the
 CC diagnosis, detection, imaging and treatment of disease, e.g. tumours,
 CC prostate cancer and breast cancer
 XX SQ Sequence 43 AA;
 Query Match 100.0%; Score 23; DB 2; Length 43;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db |||||
 7 GQPR 10
 RESULT 71
 ABG26421
 ID ABG26421 standard; protein; 43 AA.
 XX AC ABG26421;
 XX DT 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #26412.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 XX WO200175067-A2.
 XX PN 11-OCT-2001.
 XX PD 30-MAR-2001; 2001WO-US008631.
 XX PF 31-MAR-2000; 2000US-00540217.
 XX PR 23-AUG-2000; 2000US-00649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX DR WPI; 2001-639362/73.
 N-PSDB; AAS90608.
 New isolated polynucleotide and encoded polypeptides, useful in
 diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits and to assess
 biodiversity.
 Claim 20; SEQ ID NO 56780; 103pp; English.
 The invention relates to isolated polynucleotide (I) and polypeptide (II)
 sequences. (I) is useful as hybridisation probes, polymerase chain
 reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 and in recombinant production of (II). The polynucleotides are also used
 in diagnostics as expressed sequence tags for identifying expressed
 genes. (I) is useful in gene therapy techniques to restore normal
 activity of (II) or to treat disease states involving (II). (II) is
 useful for generating antibodies against it, detecting or quantitating a
 polypeptide in tissue, as molecular weight markers and as a food
 supplement. (II) and its binding partners are useful in medical imaging
 of sites expressing (II). (I) and (II) are useful for treating disorders
 involving aberrant protein expression or biological activities. The
 polypeptide and polynucleotide sequences have applications in
 diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits to assess biodiversity
 and to produce other types of data and products dependent on DNA and
 amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 amino acid sequences of the invention. Note: The sequence data for this
 patent did not appear in the printed specification, but was obtained in
 electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 43 AA;
 Query Match 100.0%; Score 23; DB 4; Length 43;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db |||||
 7 GQPR 10
 RESULT 71
 AAE21238
 ID AAE21238 standard; peptide; 43 AA.
 XX AC AAE21238;
 XX DT 01-JUL-2002 (first entry)
 XX DE Human gene 1 encoded secreted protein fragment, SEQ ID NO:103.
 XX KW Human; secreted protein; gene therapy; human immunodeficiency virus; HIV;
 KW immune disease; autoimmune disease; anaemia; multiple sclerosis; cancer;
 KW rheumatoid arthritis; hyperproliferative disorder; melanoma; neoplasm;
 KW seazy syndrome; Gaucher's disease; neurological disease; cardiac arrest;
 KW Alzheimer's disease; Parkinson's disease; Charcot-Marie-Tooth disease;
 KW cardiovascular disorder; cerebrovascular disorder; tachycardia; angina;
 KW thrombosis; ocular disorder; corneal infection; wound healing; cardiant;
 KW vascular; thrombolytic; cytostatic; nootropic.
 XX OS Homo sapiens.
 XX PN WO200216390-A1.
 XX PD 28-FEB-2002.
 XX PF 17-JAN-2001; 2001WO-US001435.
 XX PR 18-AUG-2000; 2000US-0226282P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX DR

PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;
 PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;
 PI Fiscella M, Ni J;
 XX WPI; 2002-304113/34.
 DR An isolated nucleic acid molecule (I) comprising a polynucleotide which
 XX encodes a polypeptide useful in the diagnosis and treatment of disorders
 XX e.g. immune disorders.
 XX Disclosure; Page 7; 504pp; English.
 XX AAD33692-AAD33736 represent cDNAs corresponding to 21 human secreted
 CC protein genes, and AAE21191-AAE21235 represent the proteins they encode.
 CC AAE21236-AAE21280 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 21 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of immune
 CC or autoimmune diseases e.g. AIDS (acquired immune deficiency syndrome),
 CC asthma, anaemia and rheumatoid arthritis, breast neoplasia and breast
 CC cancer, neurological diseases e.g. Alzheimer's disease, Parkinson's
 CC disease, Huntington's disease, Tourette syndrome, meningitis,
 CC demyelinating disease, peripheral neuropathies, neoplasia, trauma,
 CC congenital malformations, spinal cord injuries, toxic neuropathies
 CC induced by neurotoxins, peripheral neuropathies, multiple sclerosis,
 CC ischaemia and infarction, haemorrhages, schizophrenia, mania, dementia,
 CC depression, panic disorder, learning disabilities, ALS, altered
 CC behaviours e.g. disorders in feeding, sleep patterns, balance and
 CC perception, encephalitis, disorders in cardiovascular, neural/sensory,
 CC reproductive and digestive systems, behavioural disorders and
 CC hyperproliferative disorder. The present sequence represents human
 CC secreted protein fragment referred to in the disclosure of the invention
 XX
 XX SQ Sequence 43 AA;
 Query Match 100.0%; Score 23; DB 5; Length 43;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db ||||
 10 GQPR 13
 RESULT 72
 ADI21604
 ID ADI21604 standard; protein; 43 AA.
 XX AC ADI21604;
 XX DT 15-APR-2004 (first entry)
 XX DE Novel human polypeptide #83.
 XX forensic; nutritional source; damaged tissue; diseased tissue;
 KW myeloid cell disorder; lymphoid cell disorder;
 KW bone cartilage tissue growth; tendon tissue growth;
 KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;
 KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.
 XX Homo sapiens.
 XX OS WO2003025148-A2.
 XX PN 27-MAR-2003.
 XX PD 19-SEP-2002; 2002WO-US029964.
 XX PF 19-SEP-2001; 2001US-0323739P.
 XX PR 19-SEP-2002; 2002US-0323739P.

PR 13-SEP-2002; 2002US-00323739.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;
 PI Haley-Vicente D;
 XX WPI; 2003-354603/33.
 DR N-PSDB; ADI21384.
 XX New polynucleotides and secreted proteins, useful for treating myeloid or
 PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve
 PT tissue growth or regeneration, in wound healing, and in tissue repair and
 PT replacement.
 XX Example 3; SEQ ID NO 855; 156pp; English.
 PS The invention relates to an isolated polynucleotide encoding a
 CC polypeptide with biological activity. The polynucleotides and
 CC polypeptides are useful in diagnostics, forensics, gene mapping,
 CC identification of mutations responsible for genetic disorders and other
 CC traits, to assess biodiversity, as nutritional sources or supplements.
 CC The polynucleotides may also be used as molecular weight markers,
 CC chromosome markers or map related gene positions, or as an antigen to
 CC raise anti-DNA antibodies or elicit immune response. The polypeptides are
 CC useful for raising antibodies, as markers for tissues in which the
 CC corresponding polypeptide is expressed, for re-engineering damaged or
 CC diseased tissues, for treating myeloid or lymphoid cell disorders, in
 CC bone cartilage, tendon, ligament and/or nerve tissue growth or
 CC regeneration, in wound healing, in tissue repair and replacement, in
 CC healing of burns, incisions and ulcers, and in treating cancer. The
 CC present sequence represents the amino acid sequence of a novel human
 CC polypeptide.
 XX SQ Sequence 43 AA;
 Query Match 100.0%; Score 23; DB 7; Length 43;
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db ||||
 7 GQPR 10
 RESULT 73
 ADI21603
 ID ADI21603 standard; protein; 43 AA.
 XX AC ADI21603;
 XX DT 15-APR-2004 (first entry)
 XX DE Novel human polypeptide #82.
 XX forensic; nutritional source; damaged tissue; diseased tissue;
 KW myeloid cell disorder; lymphoid cell disorder;
 KW bone cartilage tissue growth; tendon tissue growth;
 KW ligament tissue growth; nerve tissue growth; regeneration; wound healing;
 KW tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.
 XX Homo sapiens.
 XX OS WO2003025148-A2.
 XX PN 27-MAR-2003.
 XX PD 19-SEP-2002; 2002WO-US029964.
 XX PF 19-SEP-2001; 2001US-0323739P.
 XX PR 13-SEP-2002; 2002US-00323739.


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PA (HYSE-) HYSEQ INC.
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang D;
PI Haley-Vicente D;
XX WPI; 2003-354603/33.
DR N-PSDB; ADI21383.
DR
XX
XX
XX New polynucleotides and secreted proteins, useful for treating myeloid or
PT lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve
PT tissue growth or regeneration, in wound healing, and in tissue repair and
PT replacement.
XX
XX Example 3; SEQ ID NO 854; 156pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding a
CC polypeptide with biological activity. The polynucleotides and
CC polypeptides are useful in diagnostics, forensics, gene mapping,
CC identification of mutations responsible for genetic disorders and other
CC traits, to assess biodiversity, as nutritional sources or supplements.
CC The polynucleotides may also be used as molecular weight markers,
CC chromosome markers or map related gene positions, or as an antigen to
CC raise anti-DNA antibodies or elicit immune response. The polypeptides are
CC useful for raising antibodies, as markers for tissues in which the
CC corresponding polypeptide is expressed, for re-engineering damaged or
CC diseased tissues, for treating myeloid or lymphoid cell disorders, in
CC bone cartilage, tendon, ligament and/or nerve tissue growth or
CC regeneration, in wound healing, in tissue repair and replacement, in
CC healing of burns, incisions and ulcers, and in treating cancer. The
CC present sequence represents the amino acid sequence of a novel human
CC polypeptide.
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XX Sequence 43 AA;
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Query Match 100.0%; Score 23; DB 7; Length 43;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GQPR 4
DB 7 GQPR 10
RESULT 74
AM89537
ID AM89537 standard; protein; 44 AA.
XX
AC AM89537;
DT
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen SEQ ID NO:17130.
DE
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
XX Homo sapiens.
OS
XX WO200157182-A2.
PN
XX
XX 09-AUG-2001.
PD
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PF 17-JAN-2001; 2001WO-US001354.
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XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
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 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-483426/52.
 XX N-PSDB; AAK62318.
 XX CC Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.
 XX CC Claim 11; SEQ ID NO 17130; 3071pp + Sequence Listing; English.
 XX CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For

CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 44 AA;
 Query Match 100.0%; Score 23; DB 4; Length 44;
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GQPR 4
 Db 25 GQPR 28
 RESULT 75
 AA003183
 ID AAO03183 standard; protein; 44 AA.
 XX AC AAO03183;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human polypeptide SEQ ID NO 17075.
 XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX OS Homo sapiens.
 XX PN WO200164835-A2.
 XX PD 07-SEP-2001.
 XX PF 26-FEB-2001; 2001WO-US004927.
 XX PR 28-FEB-2000; 2000US-00515126.
 XX PR 18-MAY-2000; 2000US-00577409.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT;
 DR WPI; 2001-514838/56.
 DR N-PSDB; AAI83114.
 XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 XX PS Claim 20; SEQ ID NO 17075; 1399pp + Sequence Listing; English.
 XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 44 AA;
Query Match 100.0%; Score 23; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
24.054 Million cell updates/sec

Title: US-10-731-921-3
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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	23	100.0	27	2 F70540	hypothetical prote
2	23	100.0	63	2 F98129	hypothetical prote
3	23	100.0	65	2 AE2406	hypothetical prote
4	23	100.0	67	2 F84040	hypothetical prote
5	23	100.0	89	2 T51191	small zinc finger-
6	23	100.0	89	2 T51192	small zinc finger-
7	23	100.0	90	2 AD0847	hydrogenase isoenz
8	23	100.0	90	2 S15199	hydrogenase expres
9	23	100.0	90	2 H85921	pleiotrophic effec
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11	23	100.0	91	2 AG2217	hypothetical prote
12	23	100.0	98	2 T2601	hypothetical prote
13	23	100.0	101	2 G97567	hypothetical prote
14	23	100.0	101	2 AF2788	hypothetical prote
15	23	100.0	101	2 F75500	hypothetical prote
16	23	100.0	102	2 S19733	hypothetical prote
17	23	100.0	102	2 I39621	hypothetical prote
18	23	100.0	102	2 AC1899	RNA-binding protei
19	23	100.0	104	1 ASLJSY	vpr protein - huma
20	23	100.0	106	2 G84541	hypothetical prote
21	23	100.0	109	2 H72687	hypothetical prote
22	23	100.0	109	2 C83432	conserved hypotet
23	23	100.0	115	2 T46397	hypothetical prote
24	23	100.0	115	2 AG0688	probable bacteriop
25	23	100.0	118	2 S14079	pimi protein - mou
26	23	100.0	122	2 E75464	hypothetical prote
27	23	100.0	126	2 H95343	hypothetical prote
28	23	100.0	128	2 A98346	hypothetical prote
29	23	100.0	129	2 H81809	hypothetical prote

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33	23	100.0	135	2 H84961	hypothetical prote
34	23	100.0	138	2 C72713	hypothetical prote
35	23	100.0	138	2 AB0699	probable pathogeni
36	23	100.0	139	2 T48793	hypothetical prote
37	23	100.0	139	2 T25747	hypothetical prote
38	23	100.0	139	2 AH3415	hypothetical membr
39	23	100.0	140	2 I46880	T-cell receptor be
40	23	100.0	140	2 E83391	probable ring-clea
41	23	100.0	141	2 H75383	hypothetical prote
42	23	100.0	144	2 E84219	hypothetical prote
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44	23	100.0	147	2 S76050	hypothetical prote
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57	23	100.0	166	2 AC2862	ureidoglycolate hy
58	23	100.0	166	2 H86243	hypothetical prote
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60	23	100.0	170	2 G95987	probable ureidogly
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65	23	100.0	177	2 T08126	pathogenesis-relat
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70	23	100.0	186	2 B82649	hypothetical prote
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73	23	100.0	196	2 A83008	conserved hypotet
74	23	100.0	197	2 H87446	potassium-transpor
75	23	100.0	200	2 B96902	probable NADPH-qui
76	23	100.0	201	2 F97063	surfactin biosynth
77	23	100.0	201	2 A83599	hypothetical prote
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95	23	100.0	213	2 A75471	probable nitrogen
96	23	100.0	213	2 C70943	hypothetical prote
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98	23	100.0	216	2 D72587	hypothetical prote
99	23	100.0	217	2 T47175	hypothetical prote
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102	23	100.0	218	2 F72169	A49L protein - var

103	23	100.0	218	2	T28586	16L protein - vari	176	23	100.0	277	2	S40167	hypothetical prote
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105	23	100.0	219	2	H72615	hypothetical prote	178	23	100.0	277	2	AB3642	protein yb1S precu
106	23	100.0	219	2	T37426	probable 25.1K pro	179	23	100.0	278	2	F82299	dihydropteroate sy
107	23	100.0	219	2	G42521	A41L protein - vac	180	23	100.0	278	2	E87704	hypothetical prote
108	23	100.0	219	2	JQ1778	SalF3L protein pre	181	23	100.0	278	2	S30124	hypothetical prote
109	23	100.0	219	2	G89791	conserved hypothet	182	23	100.0	279	2	T37010	transcription regu
110	23	100.0	220	2	S25245	rep protein - Bord	183	23	100.0	279	2	A02663	hypothetical prote
111	23	100.0	221	2	PQ0764	chlorophyll a/b-bi	184	23	100.0	282	2	T34934	stage 0 sporulatio
112	23	100.0	221	2	AG1961	hypothetical prote	185	23	100.0	283	2	F97357	hypothetical prote
113	23	100.0	223	2	T19194	hypothetical prote	186	23	100.0	283	2	A98340	hypothetical prote
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115	23	100.0	224	2	AH0875	probable membrane	188	23	100.0	287	2	T27056	hypothetical prote
116	23	100.0	225	2	A86043	probable transposa	189	23	100.0	289	1	G3HUW1	Ig gamma-3 heavy c
117	23	100.0	226	2	T43115	IS946 transposase	190	23	100.0	289	2	T36187	hypothetical prote
118	23	100.0	226	2	A43948	transposase - Lact	191	23	100.0	290	2	E83331	transcription regu
119	23	100.0	226	2	A34023	probable transposa	192	23	100.0	291	2	S15927	sfaH protein precu
120	23	100.0	226	2	A37751	probable transposa	193	23	100.0	293	2	G82997	probable transcrip
121	23	100.0	226	2	S25777	hypothetical prote	194	23	100.0	296	1	WMADL2	late 100K protein
122	23	100.0	227	1	H84387	probable phosphoes	195	23	100.0	297	2	T18660	hypothetical prote
123	23	100.0	227	1	S68150	eosinophil major b	196	23	100.0	297	2	B70685	hypothetical prote
124	23	100.0	228	2	T11130	cytochrome-c oxida	197	23	100.0	298	2	AG3531	high-affinity zinc
125	23	100.0	230	2	B95337	hypothetical prote	198	23	100.0	298	2	C97445	transcription regu
126	23	100.0	232	2	I46679	alpha-smooth muscl	199	23	100.0	299	2	C49233	S fimbrial adhesin
127	23	100.0	232	2	H75274	polypeptide deform	200	23	100.0	299	2	I76900	F1652 minor fibmri
128	23	100.0	232	2	T43098	transposase - Lact	201	23	100.0	300	2	G70719	hypothetical prote
129	23	100.0	233	1	A73174	probable phosphoes	202	23	100.0	303	2	A71557	probable pseudouri
130	23	100.0	233	1	H71040	probable phosphoes	203	23	100.0	304	2	H96528	hypothetical prote
131	23	100.0	234	2	PT0207	Ig gamma chain C r	204	23	100.0	305	2	T31740	hypothetical prote
132	23	100.0	237	2	B84377	hypothetical prote	205	23	100.0	307	2	H75405	probable singlet o
133	23	100.0	238	2	T27044	hypothetical prote	206	23	100.0	308	2	H70852	probable lipR prot
134	23	100.0	238	2	G83031	probable ATP-bindi	207	23	100.0	308	2	AE2359	hypothetical prote
135	23	100.0	238	2	AG3111	hypothetical prote	208	23	100.0	309	2	T47685	probable RNA bindi
136	23	100.0	243	1	H64413	probable phosphoes	209	23	100.0	310	2	AC1859	hypothetical prote
137	23	100.0	243	2	H82767	hypothetical prote	210	23	100.0	310	2	T26710	hypothetical prote
138	23	100.0	244	2	AG1013	probable exported	211	23	100.0	311	2	T15997	hypothetical prote
139	23	100.0	244	2	T33066	hypothetical prote	212	23	100.0	312	1	S74432	hypothetical prote
140	23	100.0	245	1	C65210	hypothetical 26.3	213	23	100.0	312	2	A61183	hypothetical prote
141	23	100.0	245	2	S19018	complement subcomp	214	23	100.0	313	2	G89064	hypothetical prote
142	23	100.0	245	2	S06329	chlorophyll a/b-bi	215	23	100.0	313	2	D69945	phage-related prot
143	23	100.0	245	2	S28827	chlorophyll a/b-bi	216	23	100.0	314	2	AB2409	dTDP-glucose dehyd
144	23	100.0	245	2	C91255	hypothetical prote	217	23	100.0	314	2	C70692	hypothetical prote
145	23	100.0	245	2	G86095	hypothetical prote	218	23	100.0	315	2	T47181	hypothetical prote
146	23	100.0	246	2	S00443	hypothetical prote	219	23	100.0	315	2	F98295	hypothetical prote
147	23	100.0	246	2	S17694	chlorophyll a/b-bi	220	23	100.0	316	2	S29394	l-arginase - Afric
148	23	100.0	248	2	B95334	probable transcrip	221	23	100.0	317	2	H70566	hypothetical prote
149	23	100.0	249	2	S69340	Ig heavy chain VHI	222	23	100.0	317	1	RMRBB	T-cell receptor be
150	23	100.0	250	2	JQ1881	hypothetical 27.1K	223	23	100.0	319	2	H87035	RNA polymerase sig
151	23	100.0	253	1	E75287	probable phosphoes	224	23	100.0	319	2	S61293	transcription init
152	23	100.0	254	2	G76814	hypothetical prote	225	23	100.0	320	2	T30894	lipase homolog TO
153	23	100.0	255	2	G75626	probable 3-alpha-h	226	23	100.0	322	1	A26370	arginase (EC 3.5.3
154	23	100.0	255	2	F98175	hypothetical prote	227	23	100.0	323	1	A26702	arginase (EC 3.5.3
155	23	100.0	255	4	S31866	Ig gamma-1 chain C	228	23	100.0	323	2	JC5011	transcription init
156	23	100.0	256	2	E95912	probable acetyltra	229	23	100.0	325	2	E75404	ABC transporter, A
157	23	100.0	256	2	A35340	H+-transporting tw	230	23	100.0	325	2	S75747	hypothetical prote
158	23	100.0	258	2	D95421	conserved hypothet	231	23	100.0	325	2	T18594	hypothetical prote
159	23	100.0	260	2	E83174	hypothetical prote	232	23	100.0	326	1	G2HU	Ig gamma-2 chain C
160	23	100.0	261	2	T04301	beta-expansin - ri	233	23	100.0	326	1	A96608	hypothetical prote
161	23	100.0	261	2	T59926	hypothetical prote	234	23	100.0	327	1	G4HU	Ig gamma-4 chain C
162	23	100.0	263	2	C95942	probable transcrip	235	23	100.0	327	2	T27042	hypothetical prote
163	23	100.0	263	4	I67792	probable glucosylc	236	23	100.0	330	1	GHU	Ig gamma-1 chain C
164	23	100.0	264	2	S04046	embryonic abundant	237	23	100.0	332	2	G65187	hypothetical prote
165	23	100.0	265	2	T33012	hypothetical prote	238	23	100.0	333	2	A95844	probable transcrip
166	23	100.0	265	2	A12942	conserved hypothet	239	23	100.0	334	2	S35015	regulatory protein
167	23	100.0	266	2	S60674	hypothetical prote	240	23	100.0	334	2	S74737	conserved hypothet
168	23	100.0	266	2	H83517	probable transcrip	241	23	100.0	335	2	B82220	hypothetical prote
169	23	100.0	269	2	AB2124	hypothetical prote	242	23	100.0	336	2	F89530	protein H28G03.1 f
170	23	100.0	269	2	S73616	MG374 homolog G12	243	23	100.0	338	2	B98195	hypothetical prote
171	23	100.0	271	2	P84442	hypothetical prote	244	23	100.0	338	2	AH3091	conserved hypothet
172	23	100.0	272	2	AC2037	hypothetical prote	245	23	100.0	338	2	G82643	conserved hypothet
173	23	100.0	272	2	AB2988	conserved hypothet	246	23	100.0	339	2	A30754	hypothetical prote
174	23	100.0	273	2	JQ0418	pyrrolidine-5-carbox	247	23	100.0	341	2	H90797	probable tellurium
175	23	100.0	275	1	E64117	dihydropteroate sy	248	23	100.0	341	2	A83644	hypothetical prote

249	23	100.0	342	2	S23438	hypothetical prote	342	23	100.0	429	2	B83257	folylpolyglutamate
250	23	100.0	342	2	S53663	hydrogenase-relate	323	23	100.0	433	2	B81992	NADH2 dehydrogenas
251	23	100.0	344	2	G70726	DNA-binding protei	324	23	100.0	433	2	D81222	NADH dehydrogenase
252	23	100.0	346	2	G69325	LPS glycosyltransf	325	23	100.0	434	2	AC2733	NADH ubiquinone ox
253	23	100.0	346	2	E83759	cytochrome d (bd-c	326	23	100.0	434	2	E97514	NADH dehydrogenase
254	23	100.0	349	2	C86969	Holliday junction	327	23	100.0	435	2	AC3396	NADH2 dehydrogenas
255	23	100.0	350	2	H87272	3-isopropylmalate	328	23	100.0	436	2	B70510	probable acyltrans
256	23	100.0	351	2	H81028	fatty acid/phospho	329	23	100.0	439	2	F87490	NADH dehydrogenase
257	23	100.0	351	2	F81972	probable fatty aci	330	23	100.0	441	2	E87214	hypothetical prote
258	23	100.0	354	2	B72363	3-isopropylmalate	331	23	100.0	443	2	S72905	phosphate sensor p
259	23	100.0	355	2	G95332	probable adenylate	332	23	100.0	444	2	H82821	NADH-ubiquinone ox
260	23	100.0	357	2	E82564	3-isopropylmalate	333	23	100.0	444	2	F75387	NADH dehydrogenase
261	23	100.0	358	1	JX0286	3-isopropylmalate	334	23	100.0	444	2	S64912	probable membrane
262	23	100.0	358	2	QJ2348	hypothetical 41.2K	335	23	100.0	445	1	G70647	NADH2 dehydrogenas
263	23	100.0	360	2	B83255	phosphate carrier	336	23	100.0	445	2	S76019	ATP-dependent clp
264	23	100.0	361	2	B53737	mannose-1-phosphat	337	23	100.0	445	2	QJ2264	canavalin - jack b
265	23	100.0	361	2	T01007	mannose-1-phosphat	338	23	100.0	445	2	S00281	canavalin - sword
266	23	100.0	362	2	C82572	phosphoserine amin	339	23	100.0	445	2	E70854	probable membrane
267	23	100.0	362	2	A53737	phosphate carrier	340	23	100.0	449	2	T34619	NADH2 dehydrogenas
268	23	100.0	363	2	A34959	triacylglycerol li	341	23	100.0	451	2	A70539	hypothetical prote
269	23	100.0	364	2	T47698	mannose-1-phosphat	342	23	100.0	453	2	AE0774	probable protease
270	23	100.0	366	2	E95856	hypothetical sugar	343	23	100.0	453	2	H64974	hypothetical prote
271	23	100.0	367	2	G83368	hypothetical prote	344	23	100.0	453	2	A98990	hypothetical prote
272	23	100.0	369	2	S72734	DNA-binding protei	345	23	100.0	453	2	DH5835	hypothetical prote
273	23	100.0	369	2	F69146	teichoic acid bios	346	23	100.0	454	2	HA2754	two component resp
274	23	100.0	370	2	F87638	conserved hypotet	347	23	100.0	454	2	F97535	nitrogen assimilat
275	23	100.0	371	2	S23861	hypothetical prote	348	23	100.0	454	2	T70637	hypothetical prote
276	23	100.0	374	2	S69339	Ig heavy chain v r	349	23	100.0	454	2	E70503	hypothetical prote
277	23	100.0	374	2	B54800	thin filament-asso	350	23	100.0	456	2	H86406	probable serine ca
278	23	100.0	375	2	T28710	hypothetical prote	351	23	100.0	458	2	F84746	collagenase prtC h
279	23	100.0	375	2	F75467	probable lipoprote	352	23	100.0	460	2	G24066	hypothetical prote
280	23	100.0	375	2	A46174	RNA-binding protei	353	23	100.0	460	2	T23667	hypothetical prote
281	23	100.0	376	1	ATR23	actin 3 - rice	354	23	100.0	464	2	C82046	sensor protein Cpx
282	23	100.0	376	2	G70800	probable ABC trans	355	23	100.0	464	2	C82967	probable peptidase
283	23	100.0	377	2	A23511	Ig gamma-3 chain C	356	23	100.0	464	2	AG0347	probable proteinas
284	23	100.0	377	2	A60764	Ig gamma-3 chain C	357	23	100.0	464	2	T50955	hypothetical prote
285	23	100.0	377	2	E69688	response regulator	358	23	100.0	466	1	S61292	transcription init
286	23	100.0	382	2	D75398	hypothetical prote	359	23	100.0	466	2	S62330	beta-fructofuranos
287	23	100.0	384	2	T39377	conserved hypotet	360	23	100.0	466	2	F82288	probable proteinas
288	23	100.0	384	2	AH1826	hypothetical prote	361	23	100.0	467	2	A82664	conserved hypotet
289	23	100.0	385	2	A85607	hypothetical prote	362	23	100.0	471	2	AB2266	trigger factor [im
290	23	100.0	386	2	T49275	serine C-palmitoyl	363	23	100.0	475	2	T27725	hypothetical prote
291	23	100.0	387	2	A82649	hypothetical prote	364	23	100.0	477	1	TVNVCS	protein-tyrosine k
292	23	100.0	391	2	T31251	aromatic oxygenase	365	23	100.0	477	2	G83205	probable lyase PA3
293	23	100.0	392	2	AG0226	probable exported	366	23	100.0	477	2	D82587	cationic amino aci
294	23	100.0	392	2	S72436	RNA-binding protei	367	23	100.0	478	2	A25407	interferon-induced
295	23	100.0	393	2	I53063	testicular tumor p	368	23	100.0	481	2	T32260	hypothetical prote
296	23	100.0	394	2	AB2747	lipid A-disacchari	369	23	100.0	481	2	S76115	hypothetical prote
297	23	100.0	394	2	A97528	lipid a-disacchari	370	23	100.0	482	2	E70554	hypothetical prote
298	23	100.0	394	2	T36852	probable integral	371	23	100.0	484	2	S23817	hypothetical prote
299	23	100.0	395	2	C71148	hypothetical prote	372	23	100.0	485	2	S75655	anthranilate synth
300	23	100.0	398	2	S16275	naringenin-chalcon	373	23	100.0	488	2	D70876	probable polyketid
301	23	100.0	398	2	S58190	naringenin-chalcon	374	23	100.0	488	2	I56507	histamine Hi recep
302	23	100.0	399	2	F69034	argininosuccinate	375	23	100.0	489	2	T49274	serine C-palmitoyl
303	23	100.0	402	2	T21278	hypothetical prote	376	23	100.0	489	2	T46450	hypothetical prote
304	23	100.0	403	2	G71564	hypothetical prote	377	23	100.0	497	1	G02938	probable debrisocu
305	23	100.0	406	2	T29521	hypothetical prote	378	23	100.0	497	1	O4HUD1	debrisoquine 4-hyd
306	23	100.0	408	2	D70549	hypothetical prote	379	23	100.0	497	2	F86712	di-/tripeptide tra
307	23	100.0	408	2	H87193	hypothetical prote	380	23	100.0	500	1	D31579	cytochrome P450 2D
308	23	100.0	409	2	B69147	probable FAD-linke	381	23	100.0	500	1	JC4153	cytochrome P450 2D
309	23	100.0	410	2	E72397	teichoic acid bios	382	23	100.0	500	1	JC4157	cytochrome P450 2D
310	23	100.0	411	2	I38873	hypothetical prote	383	23	100.0	500	1	JE0258	cytochrome P450 2D
311	23	100.0	412	2	S76239	serine C-palmitoyl	384	23	100.0	500	1	S16872	cytochrome P450 2D
312	23	100.0	412	2	C86177	hypothetical prote	385	23	100.0	500	1	S37284	cytochrome P450 2D
313	23	100.0	412	2	F69796	hypothetical prote	386	23	100.0	502	2	C97640	probable ATP-depen
314	23	100.0	414	2	S24154	sugar-binding, prot	387	23	100.0	502	2	A28663	dead-box ATP-depen
315	23	100.0	414	2	T38742	alanine-glyoxylate	388	23	100.0	503	2	AB2040	hypothetical prote
316	23	100.0	418	2	H83126	hypothetical prote	389	23	100.0	503	2	F95988	probable ATP-depen
317	23	100.0	420	2	AB0098	probable secretion	390	23	100.0	504	1	A26822	debrisoquine 4-hyd
318	23	100.0	425	2	AB0813	diaminopimelate de	391	23	100.0	504	1	A30247	cytochrome P450 2D
319	23	100.0	427	2	E87669	hypothetical prote	392	23	100.0	504	1	O4RTD5	cytochrome P450 2D
320	23	100.0	427	2	E96716	conserved hypotet	393	23	100.0	504	2	I49427	cytochrome P450 16
321	23	100.0	428	2	G82238	probable RNA-bindi	394	23	100.0	505	2	A32261	agarase (EC 3.2.1.

395	23	100.0	507	2	T44312	hypothetical prote	468	23	100.0	638	2	T08917	auxin response fac
396	23	100.0	509	2	AH0578	citrate (pro-3S)-1	469	23	100.0	651	2	T31175	hypothetical prote
397	23	100.0	512	1	T70506	hypothetical prote	470	23	100.0	653	2	T48270	dnak-type molecula
398	23	100.0	517	2	A49413	perilipin A - rat	471	23	100.0	653	2	T48341	endoglin - mouse
399	23	100.0	527	1	T37895	hypothetical prote	472	23	100.0	655	2	S54183	acyl-CoA dehydroge
400	23	100.0	528	1	B70531	probable sigA prot	473	23	100.0	655	2	A54872	acyl-CoA dehydroge
401	23	100.0	529	2	B24059	t complex polypept	474	23	100.0	655	2	S40521	FKBP protein - hum
402	23	100.0	532	2	S74453	hypothetical prote	475	23	100.0	661	2	F83342	probable cation-tr
403	23	100.0	533	1	TVFVFP	protein-tyrosine k	476	23	100.0	661	2	E82414	biosynthetic argin
404	23	100.0	534	2	G75348	conserved hypothet	477	23	100.0	665	2	D96621	auxin response fac
405	23	100.0	534	2	S62572	hypothetical prote	478	23	100.0	665	2	S62328	kinesin-like DNA b
406	23	100.0	537	2	T50099	probable protein-t	479	23	100.0	666	2	B70803	hypothetical prote
407	23	100.0	538	2	B83625	probable gamma-glu	480	23	100.0	668	2	C96501	hypothetical prote
408	23	100.0	546	2	D83408	hypothetical prote	481	23	100.0	670	2	C83540	conserved hypothet
409	23	100.0	548	1	H9858	bacillolysin (EC 3	482	23	100.0	673	2	AB1936	hypothetical prote
410	23	100.0	551	2	S56283	protein-tyrosine-p	483	23	100.0	677	1	CNHUB	chromogranin B pre
411	23	100.0	553	2	T45872	hypothetical prote	484	23	100.0	677	2	S70722	hypothetical prote
412	23	100.0	555	2	T48453	hypothetical prote	485	23	100.0	678	2	S77215	hypothetical prote
413	23	100.0	556	2	S10486	t-complex-type mol	486	23	100.0	681	2	H83044	2,4-dienoyl-CoA re
414	23	100.0	556	2	S13163	t-complex-type mol	487	23	100.0	688	2	T32750	hypothetical prote
415	23	100.0	556	2	JH0475	t complex polypept	488	23	100.0	690	2	H84309	protoporphyrin IX
416	23	100.0	556	2	JC1443	t complex polypept	489	23	100.0	695	2	B75295	hypothetical prote
417	23	100.0	556	2	JQ0866	t complex protein	490	23	100.0	696	2	H90798	iha adhesin (impor
418	23	100.0	560	2	JCS180	serine C-palmitoyl	491	23	100.0	696	2	G85607	probable receptor
419	23	100.0	565	2	T33851	thin filament-asso	492	23	100.0	697	2	JC2365	fused proteinase-c
420	23	100.0	567	2	JCS597	transforming growt	493	23	100.0	705	1	CIHURB	complement subcomp
421	23	100.0	571	2	T31170	maturase-related p	494	23	100.0	706	2	H81943	probable polyribon
422	23	100.0	574	2	H87036	RNA polymerase sig	495	23	100.0	707	2	C81161	polyribonucleotide
423	23	100.0	574	2	AD1863	cobalamin biosynth	496	23	100.0	708	2	T48022	hypothetical prote
424	23	100.0	575	2	AG2566	hypothetical prote	497	23	100.0	710	2	T44753	hypothetical prote
425	23	100.0	579	2	JCS955	transforming growt	498	23	100.0	713	2	S27966	probable serine/th
426	23	100.0	592	2	T42078	serine/threonine p	499	23	100.0	715	2	T02836	long chain fatty a
427	23	100.0	597	2	T01808	hypothetical prote	500	23	100.0	716	1	WVQ53	80K protein - pola
428	23	100.0	599	2	JC8009	choline dehydrogen	501	23	100.0	718	2	A83282	probable TonB-depe
429	23	100.0	603	1	DNHUN5	NADH2 dehydrogenas	502	23	100.0	721	2	B83237	probable TonB-depe
430	23	100.0	603	2	B59154	NADH2 dehydrogenas	503	23	100.0	723	2	T14765	hypothetical prote
431	23	100.0	603	2	T11516	NADH2 dehydrogenas	504	23	100.0	727	2	JC7818	metalloproteinase
432	23	100.0	603	2	T14026	NADH2 dehydrogenas	505	23	100.0	728	1	JH0579	hepatocyte growth
433	23	100.0	603	2	T14149	NADH2 dehydrogenas	506	23	100.0	729	2	S76065	hypothetical prote
434	23	100.0	603	2	T14199	NADH2 dehydrogenas	507	23	100.0	732	2	T52588	wall-associated se
435	23	100.0	603	2	T11490	NADH2 dehydrogenas	508	23	100.0	733	2	A87168	conserved hypothet
436	23	100.0	603	2	JCS183	serine C-palmitoyl	509	23	100.0	739	2	I40715	malate synthase (S
437	23	100.0	603	2	T37518	probable transcrip	510	23	100.0	741	2	AF2297	hypothetical prote
438	23	100.0	604	2	T11867	NADH2 dehydrogenas	511	23	100.0	766	1	WZBEC5	infected cell prot
439	23	100.0	604	2	T11247	NADH2 dehydrogenas	512	23	100.0	766	2	H83141	probable two-compo
440	23	100.0	604	2	T36966	hypothetical prote	513	23	100.0	772	2	T13078	KIAA0992 protein -
441	23	100.0	605	2	AI0551	maltodextrin gluco	514	23	100.0	774	1	QRECF4	iron(III) dicitrat
442	23	100.0	605	2	C64769	alpha-glucosidase	515	23	100.0	779	2	D82995	conserved hypothet
443	23	100.0	605	2	E90685	maltodextrin gluco	516	23	100.0	781	2	H95392	probable MrcB peni
444	23	100.0	605	2	A85536	maltodextrin gluco	517	23	100.0	782	2	S33945	late protein, 100K
445	23	100.0	606	1	QX805M	NADH2 dehydrogenas	518	23	100.0	784	2	H83158	Fe(III) dicitrate
446	23	100.0	606	2	T11503	NADH2 dehydrogenas	519	23	100.0	789	2	T28714	hypothetical prote
447	23	100.0	606	2	T11150	NADH2 dehydrogenas	520	23	100.0	790	2	E83621	probable TonB-depe
448	23	100.0	606	2	T11412	NADH2 dehydrogenas	521	23	100.0	791	2	T12455	hypothetical prote
449	23	100.0	606	2	C58851	NADH2 dehydrogenas	522	23	100.0	792	2	F83156	probable metal tra
450	23	100.0	606	2	S41830	NADH2 dehydrogenas	523	23	100.0	794	2	I58376	hypothetical prote
451	23	100.0	606	2	T45560	NADH2 dehydrogenas	524	23	100.0	795	2	D64343	hypothetical prote
452	23	100.0	606	2	T11373	NADH2 dehydrogenas	525	23	100.0	802	2	T45642	FtsH metalloprotei
453	23	100.0	606	2	T11257	NADH2 dehydrogenas	526	23	100.0	803	1	S35695	neurotrophin-3 rec
454	23	100.0	606	2	T11060	NADH2 dehydrogenas	527	23	100.0	815	2	B30843	glutenin high mole
455	23	100.0	606	2	S13526	hydrogenase (EC 1	528	23	100.0	815	2	JN0689	glutenin, high-mol
456	23	100.0	606	2	JCS5956	transforming growt	529	23	100.0	818	1	E64807	outer membrane ush
457	23	100.0	608	2	E84750	hypothetical prote	530	23	100.0	820	1	TVCTFP	protein-tyrosine k
458	23	100.0	608	2	T03278	gene EriIN protein	531	23	100.0	821	2	B75530	ATP-dependent prot
459	23	100.0	608	2	G02640	polycystic kidney	532	23	100.0	824	2	I50618	c-fps proto oncoge
460	23	100.0	609	1	TVMVGC	protein-tyrosine k	533	23	100.0	825	1	A40026	neurotrophin-3 rec
461	23	100.0	609	2	S26161	NADH2 dehydrogenas	534	23	100.0	825	2	A51178	neurotrophin recep
462	23	100.0	610	2	AD2632	hypothetical prote	535	23	100.0	829	2	E87305	TonB-dependent rec
463	23	100.0	611	2	T04510	hypothetical prote	536	23	100.0	830	2	S15720	glutenin high mole
464	23	100.0	613	2	T47975	auxin response fac	537	23	100.0	832	2	E84543	probable beta-gala
465	23	100.0	614	2	S27962	modulator recognit	538	23	100.0	835	2	AH1861	DNA topoisomerase
466	23	100.0	616	2	I38231	S-laminin - human	539	23	100.0	836	2	T30312	pilin biosynthetic
467	23	100.0	622	2	A84904	hypothetical prote	540	23	100.0	839	1	I73632	neurotrophin-3 rec

541	23	100.0	846	2	S52418	GTP-binding regula	614	23	100.0	1333	2	A37488	Ras guanine nucleo
542	23	100.0	846	2	H70599	hypothetical prote	615	23	100.0	1336	2	S25716	Ras guanine nucleo
543	23	100.0	847	2	C87678	TonB-dependent rec	616	23	100.0	1350	2	S89756	protein T23E7.1 [i
544	23	100.0	848	2	S02262	glutenin high mole	617	23	100.0	1355	2	T28715	hypothetical prote
545	23	100.0	848	2	E86643	probable G-protein	618	23	100.0	1355	2	T00075	hypothetical prote
546	23	100.0	852	2	I51259	tyrosine kinase C	619	23	100.0	1369	2	S58160	hypothetical prote
547	23	100.0	855	2	C82983	hypothetical prote	620	23	100.0	1425	2	T30811	hepatocyte growth
548	23	100.0	872	2	H75564	probable ATP-depen	621	23	100.0	1438	2	T17402	dihydroaeruginosic
549	23	100.0	873	1	TVFVF	protein-tyrosine k	622	23	100.0	1468	2	F96610	probable polyprote
550	23	100.0	873	1	TVFVF	protein-tyrosine k	623	23	100.0	1503	2	T43166	alpha-2-macroglobu
551	23	100.0	880	1	E64113	DNA topoisomerase	624	23	100.0	1503	2	T31418	synaptonemal compl
552	23	100.0	885	1	I38968	100 kDa coactivato	625	23	100.0	1508	2	E87696	glutamate synthase
553	23	100.0	891	2	AF2915	cell division prot	626	23	100.0	1558	2	T29253	hypothetical prote
554	23	100.0	895	2	S20582	dystrophin-associa	627	23	100.0	1571	2	T00062	hypothetical prote
555	23	100.0	900	2	F71426	hypothetical prote	628	23	100.0	1736	2	T00391	hypothetical prote
556	23	100.0	902	2	A97690	cell division prot	629	23	100.0	1797	2	A55677	laminin beta-2 cha
557	23	100.0	916	2	S60779	DNA gyrase chain A	630	23	100.0	1798	2	S53869	laminin beta-2 cha
558	23	100.0	916	2	A81089	DNA gyrase chain A	631	23	100.0	1801	1	MMRTS	laminin beta-2 cha
559	23	100.0	923	2	B81853	DNA topoisomerase	632	23	100.0	1815	2	S73021	polyketide synthas
560	23	100.0	923	2	H83248	DNA gyrase subunit	633	23	100.0	1822	2	F87203	polyketide synthas
561	23	100.0	927	2	T51536	hypothetical prote	634	23	100.0	1827	2	B70984	probable polyketid
562	23	100.0	930	2	A25923	progesterone recep	635	23	100.0	1834	1	JDMU1	DNA-directed RNA p
563	23	100.0	943	2	G83448	2-oxoglutarate den	636	23	100.0	1840	2	G85422	hypothetical prote
564	23	100.0	952	2	S32954	hypothetical prote	637	23	100.0	1896	1	RNFF2L	DNA-directed RNA p
565	23	100.0	965	2	C82560	excinuclease ABC c	638	23	100.0	2124	2	A28452	proteoglycan core
566	23	100.0	967	2	F82668	oxoglutarate dehyd	639	23	100.0	2139	2	T18296	myosin heavy chain
567	23	100.0	984	2	T44608	pyruvate carboxyla	640	23	100.0	2157	2	AI3009	peptide synthetase
568	23	100.0	998	2	T30930	hypothetical prote	641	23	100.0	2199	2	T40008	Cdc20p - fission y
569	23	100.0	1003	2	A38234	oxoglutarate dehyd	642	23	100.0	2254	2	T09053	low voltage-activa
570	23	100.0	1006	2	T00050	hypothetical prote	643	23	100.0	2295	2	C88369	protein unc-52 [im
571	23	100.0	1006	2	F96683	hypothetical prote	644	23	100.0	2327	2	T42630	aggrscan - bovine
572	23	100.0	1023	2	G96509	protein F27F5.21 [645	23	100.0	2386	1	FNHU	fibronectin precur
573	23	100.0	1040	1	A38306	alpha-mannosidase	646	23	100.0	2437	2	S53611	MIB1 protein - ra
574	23	100.0	1044	2	T43155	nitrite reductase	647	23	100.0	2472	2	E83594	still frameshift p
575	23	100.0	1044	2	T43160	conserved hypotet	648	23	100.0	2491	1	A28372	insulin-like growt
576	23	100.0	1051	2	C95367	probable calcium t	649	23	100.0	2566	2	E98274	hypothetical prote
577	23	100.0	1054	2	A61221	alkaline amylopull	650	23	100.0	2723	2	T03221	probable polyketid
578	23	100.0	1056	2	A53767	mucin MUC5B, trach	651	23	100.0	2767	1	UIHU	thyroglobulin prec
579	23	100.0	1072	2	A84112	hypothetical prote	652	23	100.0	2796	2	JC4743	fatry-acid synthas
580	23	100.0	1075	2	T31668	ncca protein - Aic	653	23	100.0	2899	2	T21546	hypothetical prote
581	23	100.0	1076	2	T31668	regulatory protein	654	23	100.0	2915	2	G87867	genome polyprotein
582	23	100.0	1090	2	A41696	probable recC prot	655	23	100.0	3175	1	RRWVEV	hypothetical prote
583	23	100.0	1097	2	D70612	probable trehalose	656	23	100.0	3375	2	T19821	tenascin-X precurs
584	23	100.0	1100	2	G83376	exodeoxyribonuclea	657	23	100.0	3566	1	A40701	Basoon protein -
585	23	100.0	1122	1	NCECVV	DNA helicase RecC	658	23	100.0	3942	2	T42730	probable tenascin
586	23	100.0	1122	2	G91088	DNA helicase RecC	659	23	100.0	4006	2	T09070	tenascin-X - bovin
587	23	100.0	1122	2	A85934	exit protein - Myc	660	23	100.0	4135	2	T42629	probable membrane
588	23	100.0	1122	2	T14180	exonuclease V chai	661	23	100.0	4910	2	S64942	cadherin-related t
589	23	100.0	1123	2	AD0865	exodeoxyribonuclea	662	23	100.0	5147	1	IJFFTM	CDA peptide synthe
590	23	100.0	1123	2	AB0125	dynenin heavy chain	663	23	100.0	7463	2	T36248	T-cell receptor be
591	23	100.0	1123	2	T30880	pyruvate carboxyla	664	20	87.0	8	2	PT0691	hypothetical prote
592	23	100.0	1146	2	AH1208	pyruvate carboxyla	665	20	87.0	26	2	S14035	hypothetical prote
593	23	100.0	1146	2	AC1565	pyruvate carboxyla	666	20	87.0	26	2	S14036	hypothetical prote
594	23	100.0	1148	2	F69685	pyruvate carboxyla	667	20	87.0	26	2	S14037	hypothetical prote
595	23	100.0	1150	2	A83978	pyruvate carboxyla	668	20	87.0	29	2	A39462	cholesterolin - do
596	23	100.0	1151	2	A45226	integrin alpha-1 c	669	20	87.0	31	2	I54515	pre-B cell Ig lamb
597	23	100.0	1155	2	T39040	hypothetical prote	670	20	87.0	34	2	F82394	hypothetical prote
598	23	100.0	1158	2	AE3285	pyruvate carboxyla	671	20	87.0	37	2	I56058	cell surface glyco
599	23	100.0	1162	2	AD3317	carbamoyl-phosphat	672	20	87.0	40	2	PQ0533	3-oxoacyl-l-acyl-ca
600	23	100.0	1171	2	T05039	hypothetical prote	673	20	87.0	53	2	S41957	naringenin-chalcon
601	23	100.0	1174	2	AE2911	pyruvate carboxyla	674	20	87.0	60	2	AD2783	hypothetical prote
602	23	100.0	1174	2	C97686	pyruvate carboxyla	675	20	87.0	60	2	E97562	hypothetical prote
603	23	100.0	1180	2	A35854	integrin alpha-1 c	676	20	87.0	63	1	GCIDC	glucagon precursor
604	23	100.0	1199	2	T29145	hypothetical prote	677	20	87.0	63	2	G69073	rubredoxin - Metha
605	23	100.0	1207	2	T00378	KIAA0641 protein	678	20	87.0	65	2	S51099	MHC class I histoc
606	23	100.0	1208	2	T00362	hypothetical prote	679	20	87.0	65	2	D84209	hypothetical prote
607	23	100.0	1238	2	S68700	HPTP beta-like tyr	680	20	87.0	65	2	B25103	ferredoxin 2[4Fe-4
608	23	100.0	1260	2	A72603	probable nitrate r	681	20	87.0	65	2	B35405	ferredoxin 2[4Fe-4
609	23	100.0	1289	2	B70748	probable smc prote	682	20	87.0	66	2	T35489	hypothetical prote
610	23	100.0	1298	1	EDB875	immediate-early pr	683	20	87.0	71	2	A40962	cAMP-dependent pro
611	23	100.0	1313	2	T29193	hypothetical prote	684	20	87.0	71	2	E83054	hypothetical prote
612	23	100.0	1317	2	T03748	apoptosis associat	685	20	87.0	72	2	E82615	hypothetical prote
613	23	100.0	1321	2	JE0352	mucin MUC5B, trach	686	20	87.0	75	2	S61573	probable membrane

687	20	87.0	76	2	T40983	hypothetical prote	760	134	2	A70315	AP4A hydrolase - A		
688	20	87.0	76	2	T45326	hypothetical prote	761	134	2	PC4214	phosphatidylethane		
689	20	87.0	80	2	F82602	conserved hypotet	762	134	2	B87632	hypothetical prote		
690	20	87.0	82	2	F96625	hypothetical prote	763	136	2	S16848	Ig lambda chain V-		
691	20	87.0	83	2	T35070	probable membrane	764	20	87.0	137	S68429	myotoxin precursor	
692	20	87.0	85	2	A87006	hypothetical prote	765	20	87.0	138	I50098	phospholipase a2 -	
693	20	87.0	85	2	T50340	hypothetical prote	766	20	87.0	138	S67968	transition protein	
694	20	87.0	86	2	T17313	hypothetical prote	767	20	87.0	139	H87488	lactoylglutathione	
695	20	87.0	87	2	S52290	HLA-A30 variant ex	768	20	87.0	139	AF0685	hypothetical prote	
696	20	87.0	88	2	B42175	tenascin homolog 3	769	20	87.0	140	PH0132	Ig lambda chain pr	
697	20	87.0	89	2	G71378	hypothetical prote	770	20	87.0	140	PH0134	Ig lambda chain pr	
698	20	87.0	91	2	S06351	excisionase - phag	771	20	87.0	140	H96923	transcription regu	
699	20	87.0	91	2	H75613	conserved hypotet	772	20	87.0	141	S40768	hypothetical prote	
700	20	87.0	92	2	B46707	CAMP-dependent pro	773	20	87.0	141	A70556	probable mutator M	
701	20	87.0	97	2	JT0703	ferredoxin-thiore	774	20	87.0	143	JQ0425	hypothetical 15.5K	
702	20	87.0	98	2	I40888	sarcosine oxidase	775	20	87.0	144	I70695	omega protein - hu	
703	20	87.0	100	2	F69133	ribosomal protein	776	20	87.0	145	S25743	Ig lambda chain -	
704	20	87.0	102	2	B83314	hypothetical prote	777	20	87.0	147	AB0900	conserved hypotet	
705	20	87.0	105	2	S22762	Ig lambda-2 chain	778	20	87.0	147	F85978	hypothetical prote	
706	20	87.0	105	2	B27390	Ig lambda-2 chain	779	20	87.0	147	C91133	hypothetical prote	
707	20	87.0	105	2	S22759	Ig lambda-2 chain	780	20	87.0	147	F65105	hypothetical prote	
708	20	87.0	106	2	S00259	Ig lambda-5 chain	781	20	87.0	147	JX0261	phospholipase A2 i	
709	20	87.0	106	2	S22760	Ig lambda-2 chain	782	20	87.0	149	S23626	Ig lambda chain V	
710	20	87.0	106	2	AC3086	sarcosine oxidase	783	20	87.0	149	S47574	BTT1 protein - yea	
711	20	87.0	106	2	F98200	sarcosine oxidase	784	20	87.0	150	C98254	probable acyl-CoA	
712	20	87.0	106	2	H75660	conserved hypotet	785	20	87.0	150	S26068	hypothetical prote	
713	20	87.0	107	2	T17856	hypothetical prote	786	20	87.0	151	S25739	Ig lambda chain -	
714	20	87.0	108	2	T29957	hypothetical prote	787	20	87.0	151	F95942	hypothetical prote	
715	20	87.0	109	2	A72546	hypothetical prote	788	20	87.0	151	E72806	gp55 protein - Myc	
716	20	87.0	112	2	AB3507	phosphoribosyl-ATP	789	20	87.0	152	F86473	hypothetical prote	
717	20	87.0	112	2	G72679	hypothetical prote	790	20	87.0	152	S76383	hypothetical prote	
718	20	87.0	113	2	A29700	Ig lambda chain V	791	20	87.0	154	1	XMECF1	flagellar protein
719	20	87.0	113	2	B54256	Ig lambda-1 chain	792	20	87.0	154	2	C90964	flagellar protein
720	20	87.0	114	2	PH0133	Ig lambda chain V	793	20	87.0	154	2	C85812	flagellar biosynth
721	20	87.0	114	2	T49338	hypothetical prote	794	20	87.0	155	2	AH0752	FlilL protein limpo
722	20	87.0	118	2	S12442	Ig lambda chain (K	795	20	87.0	155	2	B30929	flagellar protein
723	20	87.0	118	2	S12441	Ig lambda chain (K	796	20	87.0	155	2	H75075	hypothetical prote
724	20	87.0	118	2	S12440	Ig lambda chain (M	797	20	87.0	158	2	E86993	hypothetical prote
725	20	87.0	118	2	S12443	Ig lambda chain (K	798	20	87.0	160	2	E86365	ripening-induced p
726	20	87.0	118	2	A39949	Ig lambda chain J-	799	20	87.0	160	2	A10760	probable propanedi
727	20	87.0	119	2	S30526	Ig lambda chain J-	800	20	87.0	161	2	C84235	hypothetical prote
728	20	87.0	119	2	S03465	Ig lambda chain J-	801	20	87.0	162	2	E87509	conserved hypotet
729	20	87.0	120	2	S30528	Ig lambda chain V	802	20	87.0	165	2	AB2721	N-utilization subs
730	20	87.0	120	2	S30527	Ig lambda chain V	803	20	87.0	166	2	I69004	histocompatibility
731	20	87.0	120	2	S30525	Ig lambda chain V	804	20	87.0	166	2	AH2568	hypothetical prote
732	20	87.0	120	2	B90158	conserved hypotet	805	20	87.0	168	2	H90588	hypothetical prote
733	20	87.0	120	2	D83166	hypothetical prote	806	20	87.0	168	2	T45305	hypothetical prote
734	20	87.0	120	2	JC4754	hypothetical 13.6k	807	20	87.0	169	2	F97502	nusb protein (PA40
735	20	87.0	120	2	T34431	hypothetical prote	808	20	87.0	171	2	T49789	hypothetical prote
736	20	87.0	121	1	PSBGAC	phospholipase A2 (809	20	87.0	171	2	C81280	probable periplasm
737	20	87.0	121	1	PSGNAM	phospholipase A2 h	810	20	87.0	172	2	F83585	probable sigma-70
738	20	87.0	122	2	S09314	Phospholipase A2 (811	20	87.0	174	2	H96001	hypothetical prote
739	20	87.0	122	2	S29882	ribosomal protein	812	20	87.0	175	2	C75300	hypothetical prote
740	20	87.0	122	2	E85751	hypothetical prote	813	20	87.0	175	2	C72513	hypothetical prote
741	20	87.0	122	2	D90867	hypothetical prote	814	20	87.0	176	2	T46479	hypothetical prote
742	20	87.0	123	2	A53335	Na+/Ca2+-exchangin	815	20	87.0	176	2	F88535	protein B0523.3 [i
743	20	87.0	123	2	I46959	Na/Ca exchanger NA	816	20	87.0	179	2	A75019	hypothetical prote
744	20	87.0	123	2	AH2667	conserved hypotet	817	20	87.0	179	2	C71205	hypothetical prote
745	20	87.0	123	2	E97449	hypothetical prote	818	20	87.0	181	2	PT0220	Ig lambda chain V-
746	20	87.0	124	2	S25113	insulin-like growt	819	20	87.0	181	2	I79640	MHC cell surface g
747	20	87.0	124	2	D84319	30S ribosomal prot	820	20	87.0	181	2	I59188	MHC cell surface g
748	20	87.0	126	2	AG1125	B. subtilis YyAH p	821	20	87.0	182	2	A49411	human leukocyte an
749	20	87.0	128	2	S33611	naringenin-chalcon	822	20	87.0	183	2	G83642	DNA-3-methyladenin
750	20	87.0	128	2	QJ1203	hypothetical 14K p	823	20	87.0	184	2	F75481	hypothetical prote
751	20	87.0	128	2	G90436	conserved hypotet	824	20	87.0	185	2	F70479	flavodoxin - Aquif
752	20	87.0	128	2	H96614	probable myrosinas	825	20	87.0	187	2	AH0114	conserved hypotet
753	20	87.0	129	2	AH3031	acyl-CoA hydrolase	826	20	87.0	187	2	E87299	hypothetical prote
754	20	87.0	131	2	G72236	hypothetical prote	827	20	87.0	187	2	S63461	hypothetical prote
755	20	87.0	132	1	T43826	ribosomal protein	828	20	87.0	189	1	A69024	conserved hypotet
756	20	87.0	132	2	T38486	probable ribosomal	829	20	87.0	189	2	S95418	probable kdpC pota
757	20	87.0	132	2	B69489	LSU ribosomal prot	830	20	87.0	190	2	S25740	Ig lambda chain -
758	20	87.0	132	2	F84322	50S ribosomal prot	831	20	87.0	190	2	AC0619	hypothetical bacte
759	20	87.0	134	2	A75535	ribosomal protein	832	20	87.0	192	2	AF1876	hypothetical prote

833	20	87.0	193	2	E82171	DNA-3-methyladenin	906	20	87.0	233	2	S25748	Ig lambda chain -
834	20	87.0	193	2	AF1823	hypothetical prote	907	20	87.0	233	2	S25752	Ig lambda chain -
835	20	87.0	195	2	T43227	hypothetical prote	908	20	87.0	233	2	AC0463	high-affinity bran
836	20	87.0	195	2	B56688	molybdopterin bios	909	20	87.0	233	2	T35594	hypothetical prote
837	20	87.0	195	2	B85481	molybdopterin bio	910	20	87.0	233	2	F64482	hypothetical prote
838	20	87.0	195	2	A90630	molybdopterin bio	911	20	87.0	234	2	S25757	Ig lambda chain -
839	20	87.0	195	2	AE0057	molybdopterin bios	912	20	87.0	234	2	A39956	Ig lambda chain pr
840	20	87.0	196	2	AE0502	molybdopterin bios	913	20	87.0	234	2	T21495	hypothetical prote
841	20	87.0	197	2	D64148	molybdopterin bios	914	20	87.0	235	2	S05270	Ig lambda chain pr
842	20	87.0	197	2	S44735	b0523.3 protein -	915	20	87.0	235	2	S25754	Ig lambda chain -
843	20	87.0	199	2	T06871	endopeptidase Clp	916	20	87.0	235	2	S25759	Ig lambda chain -
844	20	87.0	201	2	B70416	endopeptidase Clp	917	20	87.0	235	2	S25750	Ig lambda chain -
845	20	87.0	201	2	A31484	troponin I, fast s	918	20	87.0	235	2	S25749	Ig lambda chain -
846	20	87.0	202	2	C72701	probable heme expo	919	20	87.0	235	2	S25758	Ig lambda chain -
847	20	87.0	203	2	T30493	hypothetical prote	920	20	87.0	235	2	S14675	Ig lambda chain -
848	20	87.0	203	2	AE0367	probable lipoprote	921	20	87.0	236	2	S25746	Ig lambda chain -
849	20	87.0	204	2	T25709	hypothetical prote	922	20	87.0	236	2	F63128	Ig lambda chain -
850	20	87.0	204	2	F87295	conserved hypothet	923	20	87.0	237	2	D87373	hypothetical prote
851	20	87.0	205	2	C95131	hypothetical prote	924	20	87.0	237	2	T10629	hypothetical prote
852	20	87.0	205	2	G87370	peptidyl-prolyl ci	925	20	87.0	238	2	S73858	arginine deiminase
853	20	87.0	206	2	I37529	HLA-Cw7 - human (f	926	20	87.0	239	2	T39885	hypothetical prote
854	20	87.0	206	2	I37528	HLA-Cw1 - human (f	927	20	87.0	240	2	T27629	hypothetical prote
855	20	87.0	206	2	JL0059	H-2 class I histoc	928	20	87.0	241	2	S25435	chlorophyll a/b-bi
856	20	87.0	206	2	JC0058	H-2 class I histoc	929	20	87.0	241	2	D87337	ada regulatory pro
857	20	87.0	206	2	JC7320	K562 cell-derived	930	20	87.0	242	2	B95217	choline transporte
858	20	87.0	208	2	T43385	60S ribosomal prot	931	20	87.0	242	2	A72706	hypothetical prote
859	20	87.0	208	2	T17343	hypothetical prote	932	20	87.0	242	2	D98081	hypothetical prote
860	20	87.0	209	1	A26166	Ig lambda-5 chain	933	20	87.0	243	2	S25755	Ig lambda chain -
861	20	87.0	209	2	H82561	hypothetical prote	934	20	87.0	243	2	I54459	MHC H-2K1-k - mous
862	20	87.0	210	2	T05298	hypothetical prote	935	20	87.0	244	2	B75459	sodium extrusion p
863	20	87.0	211	2	C87462	hypothetical prote	936	20	87.0	247	1	LNRBPS	pulmonary surfacta
864	20	87.0	213	2	A21177	Ig light chain pre	937	20	87.0	247	2	D72332	conserved hypothet
865	20	87.0	213	2	PC21066	Ig lambda chain V	938	20	87.0	248	1	LNDGPS	pulmonary surfacta
866	20	87.0	214	2	S21456	Ig lambda chain V	939	20	87.0	248	1	LNRTPS	pulmonary surfacta
867	20	87.0	214	2	D84808	hypothetical prote	940	20	87.0	248	2	A48853	pulmonary surfacta
868	20	87.0	214	2	H75592	conserved hypothet	941	20	87.0	248	2	T35233	hypothetical prote
869	20	87.0	215	2	T49743	probable rrm-type	942	20	87.0	249	2	H90741	molybdopterin bios
870	20	87.0	216	2	A42193	Ig lambda chain (B	943	20	87.0	249	2	AI0602	molybdopterin bios
871	20	87.0	216	2	S03401	Ig lambda chain (K	944	20	87.0	249	2	C85592	molybdopterin bios
872	20	87.0	216	2	S69130	Ig lambda chain (D	945	20	87.0	249	2	B32352	molybdopterin bios
873	20	87.0	216	2	JE0241	Ig kappa chain Am3	946	20	87.0	249	2	S07917	molybdopterin bios
874	20	87.0	216	2	S29258	Ig lambda chain V	947	20	87.0	249	2	H90048	hypothetical prote
875	20	87.0	217	2	T50004	potassium-transpor	948	20	87.0	249	2	S76552	hypothetical prote
876	20	87.0	217	2	F50627	RNA binding protei	949	20	87.0	250	2	E75376	2-hydroxyhepta-2,4
877	20	87.0	218	2	D87264	hypothetical prote	950	20	87.0	250	2	H75504	MutV/nudix family
878	20	87.0	220	2	D87535	glutathione S-tran	951	20	87.0	251	1	S35729	myb-related protei
879	20	87.0	220	2	F63218	conserved hypothet	952	20	87.0	252	2	B82181	oxidoreductase, sh
880	20	87.0	221	1	JN0489	butyrate-acetoacet	953	20	87.0	253	2	C84177	proteasome, subuni
881	20	87.0	221	2	AF3379	molybdopterin-guan	954	20	87.0	253	2	AE2021	hypothetical prote
882	20	87.0	222	2	AH2619	conserved hypothet	955	20	87.0	254	2	F83271	hypothetical prote
883	20	87.0	222	2	H97401	probable endopepti	956	20	87.0	255	2	I54307	hypothetical prote
884	20	87.0	223	2	H87335	conserved hypothet	957	20	87.0	255	2	C90431	MHC HLA-A30J5 heav
885	20	87.0	224	1	S76529	hypothetical prote	958	20	87.0	255	2	S12255	conserved hypothet
886	20	87.0	224	2	B87440	transcription regu	959	20	87.0	256	2	B95383	hypothetical prote
887	20	87.0	225	1	A64181	nrfC protein - Hae	960	20	87.0	256	2	AH1978	probable Short Cha
888	20	87.0	225	2	T36651	probable cation tr	961	20	87.0	259	2	AD3141	hypothetical prote
889	20	87.0	226	2	S25745	Ig lambda chain -	962	20	87.0	259	2	H98146	probable amino-aci
890	20	87.0	226	2	T08651	hypothetical prote	963	20	87.0	259	2	C90754	hypothetical prote
891	20	87.0	230	2	S49449	Ig lambda chain -	964	20	87.0	259	2	G64831	probable membrane
892	20	87.0	230	2	A70821	hypothetical prote	965	20	87.0	259	2	A85618	hypothetical prote
893	20	87.0	231	2	S26035	cytochrome-c oxida	966	20	87.0	260	2	A84695	probable tropinone
894	20	87.0	231	2	S25751	Ig lambda chain -	967	20	87.0	260	2	D86266	hypothetical prote
895	20	87.0	231	2	S25738	Ig lambda chain -	968	20	87.0	261	2	G70980	transcription init
896	20	87.0	232	2	S26023	cytochrome-c oxida	969	20	87.0	262	2	F72336	conserved hypothet
897	20	87.0	232	2	S25742	Ig lambda chain -	970	20	87.0	262	2	E75400	hypothetical prote
898	20	87.0	232	2	S25756	Ig lambda chain -	971	20	87.0	262	2	T27848	hypothetical prote
899	20	87.0	232	2	D75062	probable flagella-	972	20	87.0	263	1	S23009	insulin-like growt
900	20	87.0	232	2	JQ0886	hypothetical prote	973	20	87.0	264	2	T46335	molybdate-binding
901	20	87.0	232	2	C72609	hypothetical prote	974	20	87.0	265	2	AB2453	hypothetical prote
902	20	87.0	232	2	H71169	hypothetical prote	975	20	87.0	265	2	T35512	hypothetical prote
903	20	87.0	233	2	B61222	cytochrome-c oxida	976	20	87.0	265	2	T15486	hypothetical prote
904	20	87.0	233	2	S25744	Ig lambda chain -	977	20	87.0	266	1	A35037	insulin-like growt
905	20	87.0	233	2	S25747	Ig lambda chain -	978	20	87.0	266	2	G87527	peptidase, M23/M37

979 20 87.0 267 2 A75131
 980 20 87.0 268 2 A71087
 981 20 87.0 269 2 T36360
 982 20 87.0 269 2 AF3494
 983 20 87.0 269 2 AG2268
 984 20 87.0 269 2 S22781
 985 20 87.0 270 1 HLUH28
 986 20 87.0 270 1 S77085
 987 20 87.0 270 2 AC1956
 988 20 87.0 272 1 A36082
 989 20 87.0 272 2 I48600
 990 20 87.0 272 2 B22826
 991 20 87.0 273 1 HLUH28
 992 20 87.0 273 1 HLUH69
 993 20 87.0 273 2 I38509
 994 20 87.0 273 2 B64446
 995 20 87.0 273 2 C97222
 996 20 87.0 274 1 HLUH32
 997 20 87.0 274 2 I68774
 998 20 87.0 274 2 I54463
 999 20 87.0 274 2 S24439
 1000 20 87.0 274 2 AI0643

ALIGNMENTS

RESULT 1
 F70540
 Hypothetical protein RV1572c - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: F70540
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:198295987; PMID:9634230
 A:Accession: F70540
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-27 <COL>
 A:Cross-references: UNIPROT:O06618; GB:Z95586; GB:AL123456; NID:G3261785; PIDN:CAB09065.
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV1572c

Query Match 100.0%; Score 23; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 2 GQPR 5

RESULT 2
 F98129
 Hypothetical protein AGR_L18 [imported] - Agrobacterium tumefaciens (strain C58, Cerson
 C:Species: Agrobacterium tumefaciens
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: F98129
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: F98129
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-63 <KUR>

A:Cross-references: UNIPROT:Q8U521; GB:AE007870; PIDN:AAK88560.1; PID:g15158269; GSPDB:GN
 C:Genetics:
 A:Gene: AGR_L18
 A:Map position: linear chromosome

Query Match 100.0%; Score 23; DB 2; Length 63;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 9 GQPR 12

RESULT 3
 AE2406
 Hypothetical protein asl4805 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AE2406
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
 N.; Nakazaki, N.; Shampo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.;
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anas
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AE2406
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-65 <KUR>
 A:Cross-references: UNIPROT:Q8YMW9; GB:BA000019; PIDN:BA076504.1; PID:g17133942; GSPDB:GN
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: asl4805

Query Match 100.0%; Score 23; DB 2; Length 65;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 27 GQPR 30

RESULT 4
 F84040
 Hypothetical protein BH3126 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: F84040
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: AB3650; MUID:20512582; PMID:11058132
 A:Accession: F84040
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-67 <STO>
 A:Cross-references: UNIPROT:Q9K980; GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BA0684
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH3126

Query Match 100.0%; Score 23; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 58 GQPR 61

RESULT 5

T51191
small zinc finger-like protein [imported] - human
C:Species: Homo sapiens (man)
C>Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C:Accession: T51191
R:Bauer, M.F.; Brunner, M.; Hofmann, S.
submitted to the EMBL Data Library, May 1999
A:Description: Cloning and mapping of the Tim10/DDP gene family encoding small zinc finger protein
A:Reference number: Z25334
A:Accession: T51191
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <BAU>
A:Cross-references: UNIPROT:Q9Y5J7; EMBL:AF150100; PIDN:AAD40006.1
C:Genetics:
A:Gene: TIM9a

Query Match 100.0%; Score 23; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 86 GQPR 89

RESULT 6
T51192
small zinc finger-like protein [imported] - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C:Accession: T51192
R:Bauer, M.F.; Brunner, M.; Hofmann, S.
submitted to the EMBL Data Library, May 1999
A:Description: Cloning and mapping of the Tim10/DDP gene family encoding small zinc finger protein
A:Reference number: Z25334
A:Accession: T51192
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89 <BAU>
A:Cross-references: UNIPROT:Q9WV98; EMBL:AF150101; PIDN:AAD40007.1
C:Genetics:
A:Gene: Tim9a

Query Match 100.0%; Score 23; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 86 GQPR 89

RESULT 7
AD0847
hydrogenase isoenzymes formation protein HycC [imported] - Salmonella enterica subsp. en
C:Species: salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 14-Apr-2003
C:Accession: AD0847
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AD0847
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05963.1; PID:g16503934; GSPDB:GN00176
C:Genetics:

A:Gene: hycC
C:Superfamily: [NiFe]-hydrogenase maturation chaperone

Query Match 100.0%; Score 23; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 40 GQPR 43

RESULT 8
S15199
hydrogenase expression/formation protein hycC - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S15199; D65053
R:Rut, S.; Jacob, A.; Schlensog, V.; Boehm, R.; Sawers, G.; Boeck, A.
Mol. Microbiol. 5, 123-135, 1991
A:Title: Molecular characterization of an operon (hyc) necessary for the activity of the
A:Reference number: S15197; MUID:91194542; PMID:1849603
A:Accession: S15199
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <LUT>
A:Cross-references: UNIPROT:P24191; EMBL:X54543; NID:g41774; PIDN:CAA38414.1; PID:g41777
R:Blattner, P.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: D65053
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-90 <BLAT>
A:Cross-references: GB:AE000356; GB:U00096; NID:g2367153; PIDN:AACT5770.1; PID:g1789083;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: hycC
C:Superfamily: [NiFe]-hydrogenase maturation chaperone

Query Match 100.0%; Score 23; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 40 GQPR 43

RESULT 9
H85921
pleiotropic effects on 3 hydrogenase isozymes [imported] - Escherichia coli (strain O15:
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85921
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, J.
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, N.
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85921
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STO>
A:Cross-references: UNIPROT:P24191; GB:AE005174; NID:g12517180; PIDN:AAG57836.1; GSPDB:G:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: hycC
C:Superfamily: [NiFe]-hydrogenase maturation chaperone

Query Match 100.0%; Score 23; DB 2; Length 90;

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Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
   ||||
Db 40 GQPR 43

RESULT 10
H91076
hydrogenase isoenzyme HycC [imported] - Escherichia coli (strain O157:H7, substrain RIMD
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: H91076
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; PMID:11258796
A:Accession: H91076
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <HAY>
A:Cross-references: UNIPROT:P24191; GB:BA000007; PIDN:BA37007.1; PID:g13363055; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
C:Gene: EC3J584
C:Superfamily: [NifE]-hydrogenase maturation chaperone

Query Match 100.0%; Score 23; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
   ||||
Db 40 GQPR 43

RESULT 11
AG2217
hypothetical protein asr3294 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 16-Aug-2004
C:Accession: AG2217
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; PMID:11759840
A:Accession: AG2217
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <KUR>
A:Cross-references: UNIPROT:Q8YR28; GB:BA000019; PIDN:BA74993.1; PID:g17132389; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
C:Gene: asr3294
C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 100.0%; Score 23; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
   ||||
Db 51 GQPR 54

RESULT 12
D72601
hypothetical protein APES047 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix

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C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: D72601
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; PMID:99310339; PMID:10382966
A:Accession: D72601
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <KAW>
A:Cross-references: UNIPROT:Q9YCI1; DDBJ:AP000061; NID:g5104821; PIDN:BAA80266.1; PID:d1
A:Experimental source: strain K1
C:Genetics:
C:Gene: APES047
C:Superfamily: phosphoesterase, MJ0912 type; phosphoesterase core homology

Query Match 100.0%; Score 23; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
   ||||
Db 25 GQPR 28

RESULT 13
G97567
hypothetical protein AGR_C_3166 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: G97567
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A:Reference number: A97359; PMID:21608551; PMID:11743194
A:Accession: G97567
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <KUR>
A:Cross-references: UNIPROT:Q8UEN1; GB:AE007869; PIDN:AAK87496.1; PID:g15156823; GSPDB:G
C:Genetics:
C:Gene: AGR_C_3166
A:Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
   ||||
Db 45 GQPR 48

RESULT 14
AF2788
hypothetical protein Atul725 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AF2788
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:21608550; PMID:11743193
A:Accession: AF2788
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <KUR>

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A;Cross-references: UNIPROT:Q8UEM1; GB:AE008688; PIDN:AAL42724.1; PID:gl7740163; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atul725
A;Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 45 GQPR 48

RESULT 15
F75500
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: F75500
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75500
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <WHI>
A;Cross-references: UNIPROT:Q9RW85; GB:AE001917; GB:AE000513; NID:g6458281; PIDN:AAF1017
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0590
A;Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 54 GQPR 57

RESULT 16
S19733
hypothetical protein 2 - Thiobacillus versutus (fragment)
C;Species: Thiobacillus versutus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S19733
R;Ubbink, M.; van Kleef, M.A.G.; Kleinjan, D.J.; Houtink, C.W.G.; Huitema, F.; Beintema,
Eur. J. Biochem. 202, 1003-1012, 1991
A;Title: Cloning, sequencing and expression studies of the genes encoding amicyanin and
A;Reference number: S19730; MUID:92111471; PMID:1765062
A;Accession: S19733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-102 <UBB>
A;Cross-references: UNIPROT:Q56464; GB:M58001; NID:gl54632; PIDN:AAA50572.1; PID:gl54636

Query Match 100.0%; Score 23; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 27 GQPR 30

RESULT 17
I39621
vpr protein - human immunodeficiency virus type 2 (isolate ST)
N;Alternate names: orf-R protein
C;Species: human immunodeficiency virus type 2, HIV-2
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: E33943
R;Kumar, P.; Hui, H.; Kappes, J.C.; Haggarty, B.S.; Hoxie, J.A.; Arya, S.K.; Shaw, G.M.;
J. Virol. 64, 890-901, 1990
A;Title: Molecular characterization of an attenuated human immunodeficiency virus type 2
A;Reference number: A33943; MUID:90112662; PMID:2296086
A;Accession: E33943
A;Molecule type: genomic RNA
A;Residues: 1-104 <KUM>

rbpA1 protein - Anabaena variabilis
C;Species: Anabaena variabilis
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 16-Aug-2004
C;Accession: I39621
R;Sato, N.
Plant Mol. Biol. 24, 819-823, 1994
A;Title: A cold-regulated cyanobacterial gene cluster encodes RNA-binding protein and rhl
A;Reference number: I39620; MUID:94250845; PMID:8193307
A;Accession: I39621
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-102 <RES>
A;Cross-references: UNIPROT:Q44560; GB:D17710; NID:g600249; PIDN:BAA04563.1; PID:g532033
C;Genetics:
A;Gene: rbpA1
C;Superfamily: ribonucleoprotein repeat homology
P;2-69/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 100.0%; Score 23; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 39 GQPR 42

RESULT 18
AC1899
RNA-binding protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AC1899
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anab
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC1899
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-102 <KUR>
A;Cross-references: UNIPROT:Q44560; GB:BA000019; PIDN:BA072698.1; PID:gl7130086; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: rbpA1
C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein

Query Match 100.0%; Score 23; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 39 GQPR 42

RESULT 19
ASLJSY
vpr protein - human immunodeficiency virus type 2 (isolate ST)
N;Alternate names: orf-R protein
C;Species: human immunodeficiency virus type 2, HIV-2
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: E33943
R;Kumar, P.; Hui, H.; Kappes, J.C.; Haggarty, B.S.; Hoxie, J.A.; Arya, S.K.; Shaw, G.M.;
J. Virol. 64, 890-901, 1990
A;Title: Molecular characterization of an attenuated human immunodeficiency virus type 2
A;Reference number: A33943; MUID:90112662; PMID:2296086
A;Accession: E33943
A;Molecule type: genomic RNA
A;Residues: 1-104 <KUM>

A;Cross-references: UNIPROT:P20884; GB:M31113; NID:gl339798; PIDN:AAB01355.1; PID:g32575
 C;Genetics:
 A;Gene: vpr
 C;Superfamily: AIDS vpr protein
 C;Keywords: AIDS; Immunodeficiency

Query Match 100.0%; Score 23; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 86 GQPR 89

RESULT 20
 G84541
 hypothetical protein At2g16590 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: G84541
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: G84541
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-106 <STO>
 A;Cross-references: UNIPROT:Q9SI59; GB:AE002093; NID:g4589971; PIDN:AAD26488.1; GSPDB:GN
 C;Genetics:
 A;Gene: At2g16590
 A;Map position: 2

Query Match 100.0%; Score 23; DB 2; Length 106;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 55 GQPR 58

RESULT 21
 H72687
 hypothetical protein APE0920 - Aeropyrum pernix (strain K1)
 C;Species: Aeropyrum pernix
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C;Accession: H72687
 R;Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
 A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Accession: H72687
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-109 <KAW>
 A;Cross-references: UNIPROT:Q9YDU3; DDBJ:AP000060; NID:g5104188; PIDN:BAA79904.1; PID:d1
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE0920
 C;Superfamily: Aeropyrum pernix hypothetical protein APE0920

Query Match 100.0%; Score 23; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 24 GQPR 27

RESULT 22

C83432

conserved hypothetical protein in type III secretion PA1702 [imported] - Pseudomonas aer
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C;Accession: C83432
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 ; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: C83432
 A;Status: preliminary

A;Molecule type: DNA
 A;Residues: 1-109 <STO>

A;Cross-references: UNIPROT:Q9I328; GB:AE004597; GB:AE004091; NID:g9947671; PIDN:AAG05091

A;Experimental source: strain PA01
 C;Genetics:

A;Gene: PA1702

Query Match 100.0%; Score 23; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 22 GQPR 25

RESULT 23

T46397

hypothetical protein DKFZp434K0920.1 - human

C;Species: Homo sapiens (man)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C;Accession: T46397

R;Ottewaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence database, January 2000

A;Reference number: Z23031

A;Accession: T46397

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-115 <AAA>

A;Cross-references: UNIPROT:Q9NTJ7; EMBL:AL136802

A;Experimental source: adult testis; clone DKFZp434K0920

C;Genetics:

A;Note: DKFZp434K0920.1

Query Match 100.0%; Score 23; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 GQPR 4
 ||||
 Db 105 GQPR 108

RESULT 24

AG0688

probable bacteriophage baseplate protein STY1634 [imported] - Salmonella enterica subsp.

C;Species: Salmonella enterica subsp. enterica serovar Typhi

C;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AG0688

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 , S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A;Reference number: AB0502; MUID:21534947; PMID:11677608

Query Match 100.0%; Score 23; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 GQPR 4
 ||||
 Db 105 GQPR 108

A:Accession: AG0688
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-115 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD01880.1; PID:gl6502723; GSPDB:GN00176
C:Genetics:
A:Gene: STY1634

Query Match 100.0%; Score 23; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 105 GQPR 108

RESULT 25
S14079
pin1 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C:Accession: S14079
R:Saris, C.J.M.; Domen, J.; Berns, A.
EMBO J. 10, 655-664, 1991
A:Title: The pin-1 oncogene encodes two related protein-serine/threonine kinases by alternative splicing
A:Reference number: S14079; MUID:91160521; PMID:1825810
A:Accession: S14079
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <SAR>

Query Match 100.0%; Score 23; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 51 GQPR 54

RESULT 26
E75464
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: E75464
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: E75464
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-122 <WHI>
A:Cross-references: UNIPROT:Q9RV21; GB:AE001941; GB:AE000513; NID:g6458589; PIDN:AAF1046
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0879
A:Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 35 GQPR 38

RESULT 27

H95343
hypothetical protein Sma1201 [imported] - Sinorhizobium meliloti (strain 1021) magaplaasm
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: H95343
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows;
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: H95343
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-126 <KUR>
A:Cross-references: UNIPROT:Q92241; GB:AE006469; PIDN:AAK65314.1; PID:gl4523770; GSPDB:G
A:Experimental source: strain 1021, megaplasmaid pSynA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Fuhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenhof, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Sma1201
A:Genome: plasmid

Query Match 100.0%; Score 23; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 31 GQPR 34

RESULT 28
A98346
hypothetical protein AGR_L_3432 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A98346
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Mollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: A98346
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-128 <KUR>
A:Cross-references: UNIPROT:Q8URC4; GB:AE007870; PIDN:AAK90291.1; PID:gl5160318; GSPDB:G
C:Genetics:
A:Gene: AGR_L_3432
A:Map position: linear chromosome

Query Match 100.0%; Score 23; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 27 GQPR 30

RESULT 29
H81809
hypothetical protein NMA1835 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: H81809

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: H81809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <PAR>
A:Cross-references: UNIPROT:Q9JQNS; GB:AL162757; GB:AL157959; NID:G7380371; PIDN:CAB8506
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1835

Query Match 100.0%; Score 23; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 64 GQPR 67

RESULT 30
C87219
hypothetical protein [imported] - *Mycobacterium leprae*
C:Species: *Mycobacterium leprae*
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: C87219
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: C87219
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <STO>
A:Cross-references: UNIPROT:Q9CB30; GB:AL450380; NID:G13094034; PIDN:CAC31995.1; GSPDB:G
C:Genetics:
A:Gene: ML2478

Query Match 100.0%; Score 23; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 45 GQPR 48

RESULT 31
G70667
hypothetical protein Rv1871c - *Mycobacterium tuberculosis* (strain H37Rv)
C:Species: *Mycobacterium tuberculosis*
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: G70667
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70667
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-129 <COL>
A:Cross-references: UNIPROT:P95144; GB:Z83859; GB:AL123456; NID:G3261678; PIDN:CAB06142.
A:Experimental source: strain H37Rv
C:Genetics:

A:Gene: Rv1871c

Query Match 100.0%; Score 23; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 40 GQPR 43

RESULT 32
B84295
hypothetical protein Vng1407c [imported] - *Halobacterium* sp. NRC-1
C:Species: *Halobacterium* sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 12-Jul-2004
C:Accession: B84295
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of *Halobacterium* species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: B84295
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <STO>
A:Cross-references: UNIPROT:Q9HPZ1; GB:AE004437; NID:G10580910; PIDN:AAG19726.1; GSPDB:G
C:Genetics:
A:Gene: VNG1407C
C:Superfamily: thioesterase

Query Match 100.0%; Score 23; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 114 GQPR 117

RESULT 33
H84961
hypothetical protein [imported] - *Buchnera* sp. (strain APS)
C:Species: *Buchnera* sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: H84961
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp. AI
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: H84961
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-135 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: yciA; BU274

Query Match 100.0%; Score 23; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 124 GQPR 127

RESULT 34
C72713
hypothetical protein APE1122 - *Aeropyrum pernix* (strain K1)

C;Species: Aeropyrum pernix
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C;Accession: C72713
 R;Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
 A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Accession: C72713
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-138 <RAW>
 A;Cross-references: UNIPROT:Q9YVC20; DDBJ:AP000060; NID:G5104188; PIDN:BAA80107.1; PID:dl
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE1122
 C;Superfamily: Aeropyrum pernix hypothetical protein APE1122

Query Match 100.0%; Score 23; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db 109 GQPR 112

RESULT 35
 AB0699
 probable pathogenicity island effector protein sseE [imported] - Salmonella enterica sub
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AB0699
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AB0699
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-138 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD01963.1; PID:G16502805; GSPDB:GN00176
 C;Genetics:
 A;Gene: sseE

Query Match 100.0%; Score 23; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db 59 GQPR 62

RESULT 36
 T48793
 hypothetical protein 15E6.10 [imported] - Neurospora crassa
 C;Species: Neurospora crassa
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 19-May-2000
 C;Accession: T48793
 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000
 A;Reference number: Z24541
 A;Accession: T48793
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-139 <SCH>
 A;Cross-references: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.10
 A;Experimental source: cosmid contig 15E6; strain 74

C;Genetics:
 A;Gene: NCSP:15E6.10
 A;Map position: 2
 C;Superfamily: Neurospora crassa hypothetical protein 15E6.10

Query Match 100.0%; Score 23; DB 2; Length 139;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db 106 GQPR 109

RESULT 37
 T25747
 hypothetical protein F39B3.3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T25747
 R;Murray, J.
 submitted to the EMBL Data Library, August 1996
 A;Description: The sequence of C. elegans cosmid F39B3.
 A;Reference number: Z20080
 A;Accession: T25747
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-139 <MUR>
 A;Cross-references: UNIPROT:Q94221; EMBL:U67952; PIDN:AAB07576.1; GSPDB:GN00028; CESP:F39;
 A;Experimental source: strain Bristol N2; clone F39B3
 C;Genetics:
 A;Gene: CESP:F39B3.3
 A;Map position: X

Query Match 100.0%; Score 23; DB 2; Length 139;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db 38 GQPR 41

RESULT 38
 AH3415
 hypothetical membrane spanning protein BME11310 [imported] - Brucella melitensis (strain
 C;Species: Brucella melitensis
 C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
 C;Accession: AH3415
 R;DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesec Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis;
 A;Reference number: AD3252; PMID:11756688
 A;Accession: AH3415
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-139 <KUR>
 A;Cross-references: UNIPROT:Q8YG52; GB:AE008917; PIDN:AAL52491.1; PID:G17983300; GSPDB:GN
 A;Experimental source: strain 16M
 C;Genetics:
 A;Gene: BME11310
 A;Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 139;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 Db 21 GQPR 24

RESULT 39

I46880
T-cell receptor beta chain - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 23-Jul-1999
C:Accession: I46880
R:Komatsu, M.; Lamoyi, E.; Mage, R.G.
J:Immunol. 138, 1621-1626, 1987
A:Title: Genomic DNA encoding rabbit T cell receptor beta-chains: isotypes and allotypes
A:Reference number: I46880; MUID:87110733; PMID:2879869
A:Accession: I46880
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-140 <KOM>
A:Cross-references: GB:M14577; NID:g165715; PIDN:AAA82089.1; PID:g552415
C:Genetics:
A:Gene: TCRB
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 100.0%; Score 23; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 17 GQPR 20

RESULT 40

E83391
probable ring-cleaving dioxygenase PA2024 [imported] - Pseudomonas aeruginosa (strain PA
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: E83391
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: E83391
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <STO>
A:Cross-references: UNIPROT:P23205; GB:AE004629; GB:AE004091; NID:g9948028; PIDN:AA0541
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2024

Query Match 100.0%; Score 23; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 61 GQPR 64

RESULT 41

H75383
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: H75383
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: H75383
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-141 <WHI>

A:Cross-references: UNIPROT:Q9RU64; GB:AE001997; GB:AE000513; NID:g6459292; PIDN:AAF11102

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR1530

A:Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 96 GQPR 99

RESULT 42

E84219
hypothetical protein Vng0613h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84219
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omar, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: E84219
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-144 <STO>
A:Cross-references: UNIPROT:Q9HRN7; GB:AE004437; NID:g10580207; PIDN:AAG19121.1; GSPDB:G
C:Genetics:
A:Gene: VNG0613H

Query Match 100.0%; Score 23; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 106 GQPR 109

RESULT 43

F83267
conserved hypothetical protein PA3017 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: F83267
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83267
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-145 <STO>
A:Cross-references: UNIPROT:Q9HZI9; GB:AE004727; GB:AE004091; NID:g9949119; PIDN:AA0640
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3017

Query Match 100.0%; Score 23; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||

Db 90 GQPR 93

RESULT 44
S76050
hypothetical protein slr0326 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76050
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Oda, K.; Okumura, S.; Shampo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76050
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-147 <KAN>
A:Cross-references: UNIPROT:Q55533; EMBL:D63999; GB:AB001339; NID:g1001396; PIDN:BAA1002
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: *Synechocystis* hypothetical protein slr0326

Query Match 100.0%; Score 23; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 37 GQPR 40

RESULT 45
E86741
hypothetical protein yJfi [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
C:Species: *Lactococcus lactis* subsp. *lactis*
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86741
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s.
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: E86741
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <STO>
A:Cross-references: UNIPROT:Q9CH09; GB:AE005176; PID:g12723868; PIDN:AAK05031.1; GSPDB:G
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yJfi

Query Match 100.0%; Score 23; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 80 GQPR 83

RESULT 46
S74366
hypothetical protein sll0062 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S74366
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Oda, K.; Okumura, S.; Shampo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.

A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S74366
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <KAN>
A:Cross-references: UNIPROT:Q55148; EMBL:D64001; GB:AB001339; NID:g1001102; PIDN:BAA10284
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 100.0%; Score 23; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 66 GQPR 69

RESULT 47
AE2595
hypothetical protein Atu0155 [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C:Species: *Agrobacterium tumefaciens*
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AE2595
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Erage, G.; Gilllet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I.
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AE2595
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-150 <KUR>
A:Cross-references: UNIPROT:Q8UYV6; GB:AE008688; PIDN:AAL41179.1; PID:g17738479; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0155
A:Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
Db 146 GQPR 149

RESULT 48
D70677
hypothetical protein Rv3547 - *Mycobacterium tuberculosis* (strain H37RV)
C:Species: *Mycobacterium tuberculosis*
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: D70677
R:Colt, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70677
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-151 <COL>
A:Cross-references: UNIPROT:P71854; GB:282098; GB:AL123456; NID:g3261664; PIDN:CAB05059.1
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv3547

Query Match 100.0%; Score 23; DB 2; Length 151;

A:Accession: AF2936
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-161 <KUR>
A:Cross-references: UNIPROT:Q8UBC4; GB:AE008689; PIDN:AAL43908.1; PID:gl17741458; GSPDB:C
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3092
A:Map position: linear chromosome

Query Match 100.0%; Score 23; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 60 GQPR 63

RESULT 54
E69155
hypothetical protein MTH426 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69155
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: E69155
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-162 <MTH>
A:Cross-references: UNIPROT:O26526; GB:AE000827; GB:AE000666; NID:g2621489; PIDN:AAB8493
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH426
A:Start codon: GTG
C:Superfamily: Methanobacterium thermoautotrophicum hypothetical protein MTH426

Query Match 100.0%; Score 23; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 40 GQPR 43

RESULT 55
T46052
ADP-ribosylation factor-like protein T16K5.210 [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46052
R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke,
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23015
A:Accession: T46052
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-165 <RIE>
A:Cross-references: UNIPROT:Q9M2X2; EMBL:AL132965
A:Experimental source: cultivar Columbia; BAC clone T16K5
C:Genetics:
A:Map position: 3
A:Introns: 21/3; 32/3; 73/2; 127/2
A:Note: T16K5.210
C:Superfamily: ADP-ribosylation factor
F:110-113/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 23; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 54 GQPR 57

RESULT 56
B97639
hypothetical protein AGR_C_4225 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97639
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourcollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B97639
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-166 <KUR>
A:Cross-references: UNIPROT:Q8UD04; GB:AE007869; PIDN:AAK88067.1; PID:gl15157491; GSPDB:B
C:Genetics:
A:Gene: AGR_C_4225
A:Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 62 GQPR 65

RESULT 57
AC2862
ureidoglycolate hydrolase alla [imported] - Agrobacterium tumefaciens (strain C58, Dupont
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AC2862
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AC2862
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-166 <KUR>
A:Cross-references: UNIPROT:Q8UD04; GB:AE008688; PIDN:AAL43313.1; PID:gl17740804; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: alla
A:Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 62 GQPR 65

RESULT 58
H86243

hypothetical protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: H86243
 R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mafti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: H86243
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-166 <STO>
 A:Cross-references: UNIPROT:O23694; GB:AE005172; NID:g2252633; PIDN:AAB65496.1; GSPDB:GN
 C:Genetics:
 A:Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 77 GQPR 80

RESULT 59
 E75257
 molybdenum cofactor biosynthesis protein C - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
 C:Accession: E75257
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: E75257
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-168 <WHI>
 A:Cross-references: UNIPROT:Q9RRC1; GB:AE002086; GB:AE000513; NID:g6460395; PIDN:AAF1211
 C:Genetics:
 A:Experimental source: strain R1
 A:Gene: DR2571
 A:Map position: 1
 C:Superfamily: Molybdenum cofactor precursor Z biosynthesis protein MoaC

Query Match 100.0%; Score 23; DB 2; Length 168;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 17 GQPR 20

RESULT 60
 G95987
 probable ureidoglycolate hydrolase (EC 3.5.3.19) [imported] - Sinorhizobium meliloti (st
 C:Species: Sinorhizobium meliloti
 C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C:Accession: G95987
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo

A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: G95987
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-170 <KUR>
 A:Cross-references: UNIPROT:Q92UG4; GB:ALS91985; PIDN:CAC49567.1; PID:g15141054; GSPDB:GN
 A:Experimental source: strain 1021, megaplasmid pSymB
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: allA; SMD20873
 A:Genome: plasmid
 C:Keywords: hydrolase

Query Match 100.0%; Score 23; DB 2; Length 170;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 62 GQPR 65

RESULT 61
 B87593
 hypothetical protein CC2778 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: B87593
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: B87593
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-171 <STO>
 A:Cross-references: UNIPROT:Q9A4Q2; GB:AE005673; NID:g13424376; PIDN:AAK24742.1; GSPDB:GN
 C:Genetics:
 A:Gene: CC2778

Query Match 100.0%; Score 23; DB 2; Length 171;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 152 GQPR 155

RESULT 62
 T50632
 hypothetical protein DKFZp762E1511.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
 C:Accession: T50632
 R:Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.
 submitted to the Protein Sequence Database, June 2000
 A:Reference number: Z25145
 A:Accession: T50632
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-171 <AAA>
 A:Cross-references: UNIPROT:Q9NPV6; EMBL:AL359614

A:Experimental source: adult melanoma (MeWo cell line); clone DKFzp762E1511
 C:Genetics:
 A:Note: DKFzp762E1511.1

Query Match 100.0%; Score 23; DB 2; Length 171;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 26 GQPR 29

RESULT 63

B75494

conserved hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: B75494

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: B75494

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-176 <WHI>

A:Cross-references: UNIPROT:Q9RWL3; GB:AE001922; GB:AE000513; NID:g6458343; PIDN:AAF1022

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR0653

A:Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 176;

Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 128 GQPR 131

RESULT 64

F83819

hypothetical protein BH1358 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: F83819

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: F83819

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-176 <STO>

A:Cross-references: UNIPROT:Q9KDG1; GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BA050

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH1358

Query Match 100.0%; Score 23; DB 2; Length 176;

Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 162 GQPR 165

RESULT 65

T08126

pathogenesis-related protein 1 precursor - pepper

C:Species: Capsicum annuum (pepper)

C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004

C:Accession: T08126

R:Wang, B.K.; Kim, Y.J.

submitted to the EMBL Data Library, March 1998

A:Description: Molecular cloning and pathogen, ethylene and developmental dependent exper

A:Reference number: Z16370

A:Accession: T08126

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-177 <HWA>

A:Cross-references: UNIPROT:O65157; EMBL:AF053343; NID:g2981170; PIDN:AAC06244.1; PID:g2

A:Experimental source: cultivar Hanbyul

C:Superfamily: pathogenesis-related leaf protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-177/Product: pathogenesis-related protein 1 #status predicted <MAT>

Query Match 100.0%; Score 23; DB 2; Length 177;

Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 154 GQPR 157

RESULT 66

T19610

hypothetical protein C31E10.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T19610

R:Swinburne, J.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19151

A:Accession: T19610

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-177 <WIL>

A:Cross-references: UNIPROT:Q93311; EMBL:Z78539; PIDN:CAB01728.1; GSPDB:GN000028; CESP:C31

A:Experimental source: clone C31E10

C:Genetics:

A:Gene: CESP:C31E10.2

A:Map position: X

A:introns: 18/1

Query Match 100.0%; Score 23; DB 2; Length 177;

Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
 ||||
 Db 78 GQPR 81

RESULT 67

HB7430

flagellin modification protein, probable [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: HB7430

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

N, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: HB7430

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-184 <STO>

A;Cross-references: UNIPROT:Q9A897; GB:AE005673; NID:g13422832; PIDN:AAK23444.1; GSPDB:Q
C;Genetics:
A;Gene: CCL464

Query Match 100.0%; Score 23; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 150 GQPR 153

RESULT 68
T27225
ADP-ribosylation factor Y57G11C.13 [similarity] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27225
R;McMurray, A.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z20330
A;Accession: T27225
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-185 <WIL>
A;Cross-references: UNIPROT:Q18237; EMBL:Z39281; PIDN:CAB16514.1; GSPDB:GN000022; CESP:Y5
A;Experimental source: clone Y57G11C
C;Genetics:
A;Gene: CESP:Y57G11C.13
A;Map position: 4
A;Introns: 41/3; 171/1
C;Superfamily: ADP-ribosylation factor
F;130-133/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 23; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 74 GQPR 77

RESULT 69
T34807
probable transcription regulator - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T34807
R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z21557
A;Accession: T34807
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-185 <MUR>
A;Cross-references: UNIPROT:Q69909; EMBL:AL023797; PIDN:CAA19414.1; GSPDB:GN000070; SCOE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOE:SC2E1.39

Query Match 100.0%; Score 23; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 140 GQPR 143

RESULT 70
B82649

A;Cross-references: UNIPROT:Q9PCS3; GB:AE003394; GB:AE003849; NID:g9106756; PIDN:AAF8451
A;Experimental source: strain 985C
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; AJ
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., M.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1705

Query Match 100.0%; Score 23; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 13 GQPR 16

RESULT 71
T46053
ADP-ribosylation factor-like protein T16K5.220 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, I
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23015
A;Accession: T46053
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-190 <RIE>
A;Cross-references: UNIPROT:Q9M2X1; EMBL:AL132965
A;Experimental source: cultivar Columbia; BAC clone T16K5
C;Genetics:
A;Map position: 3
A;Introns: 21/3; 71/2
A;Note: T16K5.220
C;Superfamily: ADP-ribosylation factor
F;108-111/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 23; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 52 GQPR 55

RESULT 72

A75518
guanyl-specific ribonuclease SA - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: A75518
R;White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75518
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-191 <WHI>
A;Cross-references: UNIPROT:Q9RX62; GB:AE001904; GB:AE000513; NID:g6458129; PIDN:AAF1002
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0453
A;Map position: 1
C;Superfamily: ribonuclease Sa

Query Match 100.0%; Score 23; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 60 GQPR 63

RESULT 73
A83008
conserved hypothetical protein PA5104 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: A83008
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83008
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-196 <STO>
A;Cross-references: UNIPROT:Q9HU79; GB:AE004923; GB:AE004091; NID:g9951395; PIDN:AAG0848
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA5104
C;Superfamily: Yersinia pestis hypothetical protein PL09040.8

Query Match 100.0%; Score 23; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 155 GQPR 158

RESULT 74
H87446
potassium-transporting ATPase, C subunit CC1593 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 27-Oct-2003
C;Accession: H87446
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
n.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-197 <STO>
A;Cross-references: GB:AE005673; NID:gl3422988; PIDN:AAK33572.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC1593
C;Superfamily: H+/K+-exchanging ATPase subunit C

Query Match 100.0%; Score 23; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 171 GQPR 174

RESULT 75

B96902
probable NADPH-quinone reductase, YabF family [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B96902
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B96902
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-200 <KUR>
A;Cross-references: UNIPROT:Q97N20; GB:AE001437; PIDN:AAK78005.1; PID:gl5022837; GSPDB:G
C;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0018

Query Match 100.0%; Score 23; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQPR 4
|||
Db 112 GQPR 115

Search completed: May 17, 2005, 10:06:57
Job time : 35 secs

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